DECLARATION FOR PATENT APPLICATION AND POWER OF ATTORNEY

As a below named inventor, I hereby declare that my residence, post office address and citizenship are as stated below next to my name; I believe that I am the original, first and sole inventor (if only one name is listed below) or an original, first and joint inventor (if plural names are listed below) of the subject matter which is claimed and for which a patent is sought on the invention entitled "**Phenylalanine Ammonia Lyase Polypeptide and Polynucleotide Sequences and Methods of Obtaining and Using Same**," the specification of which (check one): ☒ is attached hereto (and is being filed as Express Mail Number EL564462110US); ☐ was filed as PCT International Application No. _____ on _____ and was amended under Article 19 on _____ (if applicable). I hereby state that I have reviewed and understand the contents of the above-identified specification, including the claims, as amended by any amendment(s) referred to above. I acknowledge the duty to disclose to the Patent and Trademark Office all information known to me to be material to patentability as defined in 37 C.F.R. §1.56.

I hereby claim foreign priority benefits under 35 U.S.C. §119 of any foreign application(s) for patent or inventor's certificate or of any PCT international application(s) designating at least one country other than the United States of America listed below and have also identified below any foreign application(s) for patent or inventor's certificate or any PCT international application(s) designating at least one country other than the United States of America filed by me on the same subject matter having a filing date before that of the application(s) of which priority is claimed:

(Application Serial Number)	(Country)	(Day/Month/Year Filed)	Priority Claimed ☐ Yes ☐ No
			☐ Yes ☐ No

I hereby claim the benefit under 35 U.S.C. §119(e) of any United States provisional application(s) listed below:

(Application Serial Number)	(Day/Month/Year Filed)

I hereby claim the benefit under 35 U.S.C. §120 of any United States application(s) or PCT international application(s) designating the United States of America listed below and, insofar as the subject matter of each of the claims of this application is not disclosed in the prior application(s) in the manner provided by the first paragraph of 35 U.S.C. §112, I acknowledge the duty to disclose to the Office all information known to me to be material to patentability as defined in 37 C.F.R. §1.56 which occurred between the filing date of the prior application(s) and the national or PCT international filing date of this application:

(Application Serial Number)	(Day/Month/Year Filed)	(Status-Patented, Pending or Abandoned)
PCT International Application PCT/US01/23270	24/07/2001	Pending
09/624,693	24/07/2000	Pending

I hereby declare that all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true; and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under 18 U.S.C. §1001 and that such willful false statements may jeopardize the validity of the application or any patent issued thereon.

POWER OF ATTORNEY: I hereby appoint as my attorneys, with full powers of substitution and revocation, to prosecute this application and transact all business in the Patent and Trademark Office connected therewith:

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Nate F. Scarpelli (22,320)
Michael F. Borun (25,447)
Trevor B. Joike (25,542)
Carl E. Moore, Jr. (26,487)

Richard H. Anderson (26,526)
Patrick D. Ertel (26,877)
James P. Zeller (28,491)

Jeffrey S. Sharp (31,879)
Martin J. Hirsch (32,237)
James J. Napoli (32,361)
Richard M. La Barge (32,254)
Robert M. Gerstein (34,824)

James A. Flight (37,622)
Roger A. Heppermann (37,641)
David A. Gass (38,153)
Gregory C. Mayer (38,238)
William K. Merkel (40,725)
Audrey L. Bartnicki (40,499)

Send correspondence to: Audrey L. Bartnicki

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Full Name of First or Sole Inventor Roberta K. Yoshida	Citizenship United States Citizen
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City (Zip) Buffalo Grove, 60089	City (Zip) Buffalo Grove, 60089
State or Country Illinois	State or Country Illinois
Date ☒ 8.22.01	Signature ☒ Roberta K. Yoshida

Second Joint Inventor, if any Anna B. Kootstra	Citizenship United States Citizen
Residence Address - Street 420 Channel Drive	Post Office Address - Street 420 Channel Drive
City (Zip) Island Lake, 60042	City (Zip) Island Lake, 60042
State or Country Illinois	State or Country Illinois
Date ☒ 8-22-01	Signature ☒ Anna Kootstra

PATENT
Attorney Docket No. 29479/500NSCA

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Applicants: Yoshida *et al.* Serial No.: unassigned Filed: August 24, 2001 For: Phenylalanine Ammonia Lyase Polypeptide and Polynucleotide Sequences and Methods of Obtaining and Using Same Group Art Unit: unassigned Examiner: unassigned	I hereby certify that this paper and all documents referred to therein as being enclosed are being deposited with the United States Postal Service on August 24, 2001, in an envelope addressed to the Assistant Commissioner for Patents, Washington, D.C. 20231 utilizing the "Express Mail Post Office to Addressee" service of the United States Postal Service under Mailing Label No. EL564462110US: Michael J. Hauman

DECLARATION OF BIOLOGICAL DEPOSIT
IN COMPLIANCE WITH THE BUDAPEST TREATY

Commissioner for Patents
Washington, D.C. 20231

Dear Sir or Madam:

Audrey L.Bartnicki, hereby states as follows:

1. I am an attorney of record for the above-identified patent application, and as such I am authorized to act on behalf of PCBU SERVICES, INC., the assignee of the application, having its principal place of business at 300 Delaware Avenue, 9th Floor-5403,Wilmington, DE 19801.

2. PCBU SERVICES, INC. is the assignee of the above-identified patent application as evidenced by an assignment dated August 3, 2001, from the co-inventors, Roberta K. Yoshida and Anna B. Kootstra, which was filed herewith for recordation in the U.S. Patent and Trademark Office.

3. The following strain, described in the specification of the above-identified application at page 68, lines 26-29, was deposited with the American Type Culture Collection, 10801 University Boulevard, Manassas, VA 20110-2209 under the terms of the Budapest Treaty:

Original Strain Name	**ATCC Strain Name**	**Date of Deposit**
RY624 (*i.e.*, plasmid pY141 introduced into *E. coli* XL1-Blue)	PTA-2224	July 12, 2000

A copy of the "Receipt in the Case of an Original Deposit Issued Pursuant to Rule 7.3 and Viability Statement Issued Pursuant to Rule 10.2" is appended.

4. The American Type Culture Collection is a depository in accordance with the Budapest Treaty for the above-deposited cultures. Should the cells mutate, become non-viable, non-functional, or be inadvertently destroyed, the assignee will replace such cells for at least thirty years from the date of the original deposit, or for at least five years from the date of the most recent request for release of a sample, or for the enforceable life of any patent issued on the above-identified application, whichever period is longest.

5. The deposit has been made under conditions of assurance of (a) ready accessibility thereto by the public if an enforceable patent is granted whereby all restrictions to the availability to the public of the cell lines so deposited will be irrevocably removed upon the granting of the patent, and (b) access to the cell lines will be available during pendency of the patent application to one determined by the Commissioner for Patents to be entitled thereto under applicable statutes and regulations.

6. All statements made herein of my own knowledge are true and all statements made on information and belief are believed to be true; and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both under section 1001 of Title 18 of the

United States Code, and that such willful false statements may jeopardize the validity of the application or any patent issued thereon.

MARSHALL, GERSTEIN & BORUN

August 24, 2001

By Audrey L. Bartnicki

Audrey L. Bartnicki, Ph.D., J.D.
Reg. No. 40,499
Attorney for Applicants

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UNITED STATES PATENT AND TRADEMARK OFFICE
DOCUMENT CLASSIFICATION BARCODE SHEET

Sequence Listing

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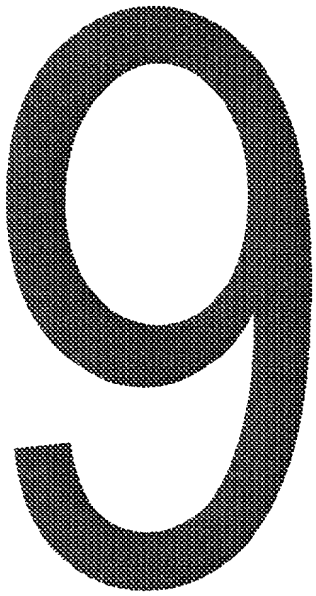

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Ala Pro Thr Lys Ser Ala Ala Gly Pro Thr Ser Ala Leu Arg Arg Thr
        25                  30                  35

ccc ggc ctc gat ggc cac gcc gcg cac cag tcg cag ctc gag atc gtg   198
Pro Gly Leu Asp Gly His Ala Ala His Gln Ser Gln Leu Glu Ile Val
    40                  45                  50

cag gag ctc ctc agc gac ccc acc gac gac gtc gtc gag ctc agc ggg   246
Gln Glu Leu Leu Ser Asp Pro Thr Asp Asp Val Val Glu Leu Ser Gly
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Tyr Ser Leu Thr Val Arg Asp Val Val Gly Ala Ala Arg Lys Gly Arg
                75                  80                  85

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Arg Val Arg Val Gln Asn Asp Asp Glu Ile Arg Ala Arg Val Asp Lys
            90                  95                  100

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Ser Val Asp Phe Leu Lys Ala Gln Leu Gln Asn Ser Val Tyr Gly Val
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acc acg ggt ttc ggt ggc tcg gcc gac acg agg act gag gat gca gtc   438
Thr Thr Gly Phe Gly Gly Ser Ala Asp Thr Arg Thr Glu Asp Ala Val
    120                 125                 130

agc ctc cag aag gcg ctc atc gag cac cag ctc tgc ggc gtg acg ccg   486
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135                 140                 145                 150

acg tcc gyc tcg tcc ttc agc gtc gga cgc ggc ctc gag aac acg ctt   534
Thr Ser Xaa Ser Ser Phe Ser Val Gly Arg Gly Leu Glu Asn Thr Leu
                155                 160                 165

ccg ctc gag gtc gtc cgc ggc gcc atg gtc atc cgc gtc aac tcg ctc   582
Pro Leu Glu Val Val Arg Gly Ala Met Val Ile Arg Val Asn Ser Leu
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atc tcg gcg tcg ggc gac ctc agc ccg ctc tcg tac atc gcc ggc gcc   726
Ile Ser Ala Ser Gly Asp Leu Ser Pro Leu Ser Tyr Ile Ala Gly Ala
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atc acc ggt cac ccc gac gtc aag gtt cac gtt ttg cac gag gga acc   774
Ile Thr Gly His Pro Asp Val Lys Val His Val Leu His Glu Gly Thr
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gag aag atc atg ttt gcg cgc gag gcc atc tcg ctc ttt ggt ctc gag   822
Glu Lys Ile Met Phe Ala Arg Glu Ala Ile Ser Leu Phe Gly Leu Glu
            250                 255                 260

gca gtc gtc ctc ggc ccg aag gag ggt ctc ggt ctg gtc aac gga acg   870
Ala Val Val Leu Gly Pro Lys Glu Gly Leu Gly Leu Val Asn Gly Thr
        265                 270                 275

gcc gtc tcc gcc tcg atg gcg acc ctc agt ctg cac gac tcg cac atg   918
Ala Val Ser Ala Ser Met Ala Thr Leu Ser Leu His Asp Ser His Met
    280                 285                 290

ctc tcg ctc ctc tcg cag gcc ttg acg gct ctc acg gtg gag gcc atg   966
Leu Ser Leu Leu Ser Gln Ala Leu Thr Ala Leu Thr Val Glu Ala Met
295                 300                 305                 310

gtc ggc cag cag ggc tcg ttc gcg ccg ttc atc cac gac gtc tgc cgc   1014
Val Gly Gln Gln Gly Ser Phe Ala Pro Phe Ile His Asp Val Cys Arg
                315                 320                 325

ccg cac ccc ggc cag gtc gag gtc gcg cgc aac atc cgc acg ctc ctt   1062
Pro His Pro Gly Gln Val Glu Val Ala Arg Asn Ile Arg Thr Leu Leu
            330                 335                 340

tcc ggc tcg tcg ttt gcc gtt gag cac gag gag gag gtc aag gtc aag   1110
Ser Gly Ser Ser Phe Ala Val Glu His Glu Glu Glu Val Lys Val Lys
        345                 350                 355

gac gac gag ggc att ctt cgc cag gac cgc tac ccg ctc cgc acg tcg   1158
Asp Asp Glu Gly Ile Leu Arg Gln Asp Arg Tyr Pro Leu Arg Thr Ser
    360                 365                 370

cct cag ttc ctc ggc ccg ctc gtg gag gac atg atg cac gcc tac tcg   1206
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gtc gag aac aag cag acc gcg cac ggc ggc aac ttc cag gcg tcg gct   1302
Val Glu Asn Lys Gln Thr Ala His Gly Gly Asn Phe Gln Ala Ser Ala
            410                 415                 420

gtc tcg att tcg atg gag aag acc agg ctc gca ctc gcc ctc atc ggc   1350
Val Ser Ile Ser Met Glu Lys Thr Arg Leu Ala Leu Ala Leu Ile Gly
        425                 430                 435

aag ctc aac ttc acg cag tgc acc gag ttg ctc aac gct gcc atg aac   1398
Lys Leu Asn Phe Thr Gln Cys Thr Glu Leu Leu Asn Ala Ala Met Asn
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cgc ggc ctg cct tcg tgc ctc gct gcc gag gac ccg tcg ctc aac tat   1446
Arg Gly Leu Pro Ser Cys Leu Ala Ala Glu Asp Pro Ser Leu Asn Tyr
455                 460                 465                 470

cac ggc aag ggc ttg gac att cac atc gct gct tac gct tcg gag ctc   1494
His Gly Lys Gly Leu Asp Ile His Ile Ala Ala Tyr Ala Ser Glu Leu
                475                 480                 485

ggc cac ctt gcc aac ccg gtc act acc ttc gtc cag ccc gca gag atg   1542
Gly His Leu Ala Asn Pro Val Thr Thr Phe Val Gln Pro Ala Glu Met
            490                 495                 500

ggc aac cag gcc gtc aac tcg ctc gct ctc atc tcc gcg cgc cgc act   1590
Gly Asn Gln Ala Val Asn Ser Leu Ala Leu Ile Ser Ala Arg Arg Thr
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gcc gag gcc aac gac gtc ctt tct ctc ctt ctc gcc tcg cac ctg tac   1638
Ala Glu Ala Asn Asp Val Leu Ser Leu Leu Leu Ala Ser His Leu Tyr
    520                 525                 530

tgc acg ctc cag gcc gtc gac ctc cgc gcg atg gag ctc gac ttc aag   1686
Cys Thr Leu Gln Ala Val Asp Leu Arg Ala Met Glu Leu Asp Phe Lys
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His Asp Ala Phe Ser Tyr Ala Thr Gly Thr Val Val Glu Leu Leu Ser
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Ser Ser Pro Ser Ala Asn Val Thr Leu Thr Ala Val Asn Ala Trp Lys
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Val Ala Ser Ala Glu Lys Ala Ile Ser Leu Thr Arg Glu Val Arg Asn
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Ser Pro Arg Thr Arg Val Leu Tyr Ser Phe Val Arg Glu Glu Leu Gly
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Val Gln Ala Arg Arg Gly Asp Val Phe Val Gly Val Gln Gln Glu Thr
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Ile Asn His Val Leu Val Lys Met Leu Ala
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Val Val Glu Leu Ser Gly Tyr Ser Leu Thr Val Arg Asp Val Val Gly
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Gly Leu Glu Asn Thr Leu Pro Leu Glu Val Val Arg Gly Ala Met Val
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                  Met Gly Leu Asp Asn Ser Lys Asn Thr Ala Lys
                    1               5                  10

ttt ttt gac cta cca aaa gcc gtc cat ggt atg aat ggt aca acc ccc   98
Phe Phe Asp Leu Pro Lys Ala Val His Gly Met Asn Gly Thr Thr Pro
            15                  20                  25

gtc aat ggt ttt aaa gcg aca gcg ctt tcc aag gcc tcc cga aca atg   146
Val Asn Gly Phe Lys Ala Thr Ala Leu Ser Lys Ala Ser Arg Thr Met
        30                  35                  40

acc aag act agc gca ctc tcg caa ttc tta gaa gcg tac cgt gaa ctc   194
Thr Lys Thr Ser Ala Leu Ser Gln Phe Leu Glu Ala Tyr Arg Glu Leu
    45                  50                  55

gag ggc tac aag aat ggt aga gcc atc aag gtt gac ggt caa acg tta   242
Glu Gly Tyr Lys Asn Gly Arg Ala Ile Lys Val Asp Gly Gln Thr Leu
60                  65                  70                  75

tct att gca gcc gtc gct gca gct gct cgc tac aat gcg gcc gtt gag   290
Ser Ile Ala Ala Val Ala Ala Ala Ala Arg Tyr Asn Ala Ala Val Glu
                80                  85                  90

ttg gac gaa tcc cca ctt gtt aag gag cgc gtg agg aaa agt cag ctt   338
Leu Asp Glu Ser Pro Leu Val Lys Glu Arg Val Arg Lys Ser Gln Leu
            95                  100                 105

gct atc gca aac aaa gta tcg acc ggt gcc agc gta tac gga ctg tca   386
Ala Ile Ala Asn Lys Val Ser Thr Gly Ala Ser Val Tyr Gly Leu Ser
        110                 115                 120

act ggt ttc ggt ggc agt gct gat aca cgg acg gac aaa ccg atg ttg   434
Thr Gly Phe Gly Gly Ser Ala Asp Thr Arg Thr Asp Lys Pro Met Leu
    125                 130                 135

ttg ggg ttt gcc ctt ttg caa cac caa cat gta ggg ata ctg ccc acc   482
Leu Gly Phe Ala Leu Leu Gln His Gln His Val Gly Ile Leu Pro Thr
140                 145                 150                 155
```

```
tcg act gag cct ttg gac gtc cta cct ctc caa gat gca aat aac aca   530
Ser Thr Glu Pro Leu Asp Val Leu Pro Leu Gln Asp Ala Asn Asn Thr
                160                 165                 170

agc atg cca gag gcg tgg att cgc ggg gcc att ttg atc cgt atg aat   578
Ser Met Pro Glu Ala Trp Ile Arg Gly Ala Ile Leu Ile Arg Met Asn
            175                 180                 185

tcg cta att cgt ggc cac tct gga atc aga tgg gag ttg atc gaa aag   626
Ser Leu Ile Arg Gly His Ser Gly Ile Arg Trp Glu Leu Ile Glu Lys
        190                 195                 200

atg aga gaa cta ctc gcg gcc aat gtg ata cct gtc gtt ccc ctg aga   674
Met Arg Glu Leu Leu Ala Ala Asn Val Ile Pro Val Val Pro Leu Arg
    205                 210                 215

ggc agc atc tcc tca tcc gga gat ctg tct ccc cta tcc tat atc gca   722
Gly Ser Ile Ser Ser Ser Gly Asp Leu Ser Pro Leu Ser Tyr Ile Ala
220                 225                 230                 235

ggc acg att att ggc aac cca tca atc aag gta tat cac ggt cca tca   770
Gly Thr Ile Ile Gly Asn Pro Ser Ile Lys Val Tyr His Gly Pro Ser
                240                 245                 250

aag tcc gga att cgc caa att gga tcc tcg aag gat gtc ttg gct ctg   818
Lys Ser Gly Ile Arg Gln Ile Gly Ser Ser Lys Asp Val Leu Ala Leu
            255                 260                 265

cat aat atc gaa cct ttc cca ctg gaa tcg aaa gaa cct ctt ggt att   866
His Asn Ile Glu Pro Phe Pro Leu Glu Ser Lys Glu Pro Leu Gly Ile
        270                 275                 280

ttg aat ggg acc gca ttc tcg gca tct gtg gca gct tta gcc cta aac   914
Leu Asn Gly Thr Ala Phe Ser Ala Ser Val Ala Ala Leu Ala Leu Asn
    285                 290                 295

gaa gct atc cat ctt gtc ttg ttg gct caa gtg tgc acg gct atg ggg   962
Glu Ala Ile His Leu Val Leu Leu Ala Gln Val Cys Thr Ala Met Gly
300                 305                 310                 315

acc gag gca ttg ata ggc act cgc gct tct cat gca ccg ttc att cat  1010
Thr Glu Ala Leu Ile Gly Thr Arg Ala Ser His Ala Pro Phe Ile His
                320                 325                 330

gcc acc gca cga cca cat ccc ggt caa gta gaa tgt gct gag aac att  1058
Ala Thr Ala Arg Pro His Pro Gly Gln Val Glu Cys Ala Glu Asn Ile
            335                 340                 345
```

```
tgg aat ttg ctc gat ggg agt aaa ttg gct cag tta gaa gag cac gaa   1106
Trp Asn Leu Leu Asp Gly Ser Lys Leu Ala Gln Leu Glu Glu His Glu
        350                 355                 360

gtt cgc cta gaa gac gat aaa tac acc ctt cgg cag gac cgt tat cca   1154
Val Arg Leu Glu Asp Asp Lys Tyr Thr Leu Arg Gln Asp Arg Tyr Pro
    365                 370                 375

ctc cga act tcg cct caa ttc ctt ggg cct cag att gaa gac ata atc   1202
Leu Arg Thr Ser Pro Gln Phe Leu Gly Pro Gln Ile Glu Asp Ile Ile
380                 385                 390                 395

tcc gct ttc cag act gta acg cag gag tgt aat tac tta cca gct act   1250
Ser Ala Phe Gln Thr Val Thr Gln Glu Cys Asn Tyr Leu Pro Ala Thr
                400                 405                 410

gac aat cca ctg att gat ggg gag act ggc gaa tct cac cac ggt ggc   1298
Asp Asn Pro Leu Ile Asp Gly Glu Thr Gly Glu Ser His His Gly Gly
            415                 420                 425

aat ttc caa gcg atg gct gta act aat gca atg gag aag acg cga ctt   1346
Asn Phe Gln Ala Met Ala Val Thr Asn Ala Met Glu Lys Thr Arg Leu
        430                 435                 440

gct tta cat cac gtt ggc aaa tta cta ttt tcc cag agc act gaa tta   1394
Ala Leu His His Val Gly Lys Leu Leu Phe Ser Gln Ser Thr Glu Leu
    445                 450                 455

gtc aat cct gcg atg aac cgc ggt ctg ccg cct tca gta gct gcc aca   1442
Val Asn Pro Ala Met Asn Arg Gly Leu Pro Pro Ser Val Ala Ala Thr
460                 465                 470                 475

gat cca tct ctc aac tac cac gcc aaa gga cta gac ata gca act gcg   1490
Asp Pro Ser Leu Asn Tyr His Ala Lys Gly Leu Asp Ile Ala Thr Ala
                480                 485                 490

gcc tac gta gcc gaa gcg act cct ggc ccc act cac att cag tcg gca   1538
Ala Tyr Val Ala Glu Ala Thr Pro Gly Pro Thr His Ile Gln Ser Ala
            495                 500                 505

gaa atg cac aac caa gct gtt aac tcc ctg gcg ttg att tct gct cgg   1586
Glu Met His Asn Gln Ala Val Asn Ser Leu Ala Leu Ile Ser Ala Arg
        510                 515                 520

gct acc atc aca tcg ttg gaa gtg cta aca tct ctg atc gcg tct tac   1634
Ala Thr Ile Thr Ser Leu Glu Val Leu Thr Ser Leu Ile Ala Ser Tyr
    525                 530                 535
```

```
ttg tat att cta tgc caa gct ctc gac ctc cgt gcc ctt cag cgc gag   1682
Leu Tyr Ile Leu Cys Gln Ala Leu Asp Leu Arg Ala Leu Gln Arg Glu
540                 545                 550                 555

ttc ttg ccc ggt cta gac atc atc att cgt gag gag tta aga tcg tca   1730
Phe Leu Pro Gly Leu Asp Ile Ile Ile Arg Glu Glu Leu Arg Ser Ser
                560                 565                 570

ttt gga tct ttc ctg tca tca gaa cag atg gag aaa ttg caa caa aat   1778
Phe Gly Ser Phe Leu Ser Ser Glu Gln Met Glu Lys Leu Gln Gln Asn
            575                 580                 585

cta act agt gca ttt gaa gat cat ctt gac aag acc acg aca atg gat   1826
Leu Thr Ser Ala Phe Glu Asp His Leu Asp Lys Thr Thr Thr Met Asp
        590                 595                 600

aat act gat cga atg act acg atg gct gct aca tca tca tca gtt cta   1874
Asn Thr Asp Arg Met Thr Thr Met Ala Ala Thr Ser Ser Ser Val Leu
    605                 610                 615

ctt caa ttc ttt act gat tct ggc gcg tct gtt cct ccc tcg tct tgc   1922
Leu Gln Phe Phe Thr Asp Ser Gly Ala Ser Val Pro Pro Ser Ser Cys
620                 625                 630                 635

gat ctt ctc tcc agt gtc tcg tcc ttc caa tct tct gtg gcg aca cgg   1970
Asp Leu Leu Ser Ser Val Ser Ser Phe Gln Ser Ser Val Ala Thr Arg
                640                 645                 650

tct tca gtt ctc atg gat gac cta cgg aaa gaa tat att ttt gga gac   2018
Ser Ser Val Leu Met Asp Asp Leu Arg Lys Glu Tyr Ile Phe Gly Asp
            655                 660                 665

cgt ggc ccc acg ccc gca agc caa tac atc gga aag aca cgg cca gta   2066
Arg Gly Pro Thr Pro Ala Ser Gln Tyr Ile Gly Lys Thr Arg Pro Val
        670                 675                 680

tac caa ttc att aga aca act ata ggc gtt cgt aag cat ggt tct gag   2114
Tyr Gln Phe Ile Arg Thr Thr Ile Gly Val Arg Lys His Gly Ser Glu
    685                 690                 695

aac tac aac aag ttt tat aat ggg ctg ggt gtc gaa gac gtt acc atc   2162
Asn Tyr Asn Lys Phe Tyr Asn Gly Leu Gly Val Glu Asp Val Thr Ile
700                 705                 710                 715

ggt caa aat ata tca cgc ata tac gag tca atc cgg gac ggc aaa atg   2210
Gly Gln Asn Ile Ser Arg Ile Tyr Glu Ser Ile Arg Asp Gly Lys Met
                720                 725                 730
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caa tcc att att gtc tcg ttg ttt gat taggtcttga aagcttgtat 2257
Gln Ser Ile Ile Val Ser Leu Phe Asp
735 740

cttattaata accatacact tcctcgaggt ctaaaaaaaa aaaaaaaaaa aaaa 2311

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Lys Ala Val His Gly Met Asn Gly Thr Thr Pro Val Asn Gly Phe Lys
20 25 30

Ala Thr Ala Leu Ser Lys Ala Ser Arg Thr Met Thr Lys Thr Ser Ala
35 40 45

Leu Ser Gln Phe Leu Glu Ala Tyr Arg Glu Leu Glu Gly Tyr Lys Asn
50 55 60

Gly Arg Ala Ile Lys Val Asp Gly Gln Thr Leu Ser Ile Ala Ala Val
65 70 75 80

Ala Ala Ala Ala Arg Tyr Asn Ala Ala Val Glu Leu Asp Glu Ser Pro
85 90 95

Leu Val Lys Glu Arg Val Arg Lys Ser Gln Leu Ala Ile Ala Asn Lys
100 105 110

Val Ser Thr Gly Ala Ser Val Tyr Gly Leu Ser Thr Gly Phe Gly Gly
115 120 125

Ser Ala Asp Thr Arg Thr Asp Lys Pro Met Leu Leu Gly Phe Ala Leu
130 135 140

Leu Gln His Gln His Val Gly Ile Leu Pro Thr Ser Thr Glu Pro Leu
145 150 155 160

Asp Val Leu Pro Leu Gln Asp Ala Asn Asn Thr Ser Met Pro Glu Ala
165 170 175

Trp Ile Arg Gly Ala Ile Leu Ile Arg Met Asn Ser Leu Ile Arg Gly
180 185 190

His Ser Gly Ile Arg Trp Glu Leu Ile Glu Lys Met Arg Glu Leu Leu
195 200 205

Ala Ala Asn Val Ile Pro Val Val Pro Leu Arg Gly Ser Ile Ser Ser
210 215 220

Ser Gly Asp Leu Ser Pro Leu Ser Tyr Ile Ala Gly Thr Ile Ile Gly
225 230 235 240

Asn Pro Ser Ile Lys Val Tyr His Gly Pro Ser Lys Ser Gly Ile Arg
245 250 255

Gln Ile Gly Ser Ser Lys Asp Val Leu Ala Leu His Asn Ile Glu Pro
260 265 270

Phe Pro Leu Glu Ser Lys Glu Pro Leu Gly Ile Leu Asn Gly Thr Ala
275 280 285

Phe Ser Ala Ser Val Ala Ala Leu Ala Leu Asn Glu Ala Ile His Leu
290 295 300

Val Leu Leu Ala Gln Val Cys Thr Ala Met Gly Thr Glu Ala Leu Ile
305 310 315 320

Gly Thr Arg Ala Ser His Ala Pro Phe Ile His Ala Thr Ala Arg Pro
325 330 335

His Pro Gly Gln Val Glu Cys Ala Glu Asn Ile Trp Asn Leu Leu Asp
340 345 350

Gly Ser Lys Leu Ala Gln Leu Glu Glu His Glu Val Arg Leu Glu Asp
355 360 365

Asp Lys Tyr Thr Leu Arg Gln Asp Arg Tyr Pro Leu Arg Thr Ser Pro
370 375 380

Gln Phe Leu Gly Pro Gln Ile Glu Asp Ile Ile Ser Ala Phe Gln Thr
385 390 395 400

Val Thr Gln Glu Cys Asn Tyr Leu Pro Ala Thr Asp Asn Pro Leu Ile
405 410 415

Asp Gly Glu Thr Gly Glu Ser His His Gly Gly Asn Phe Gln Ala Met
420 425 430

Ala Val Thr Asn Ala Met Glu Lys Thr Arg Leu Ala Leu His His Val
435 440 445

Gly Lys Leu Leu Phe Ser Gln Ser Thr Glu Leu Val Asn Pro Ala Met
450 455 460

Asn Arg Gly Leu Pro Pro Ser Val Ala Ala Thr Asp Pro Ser Leu Asn
465 470 475 480

Tyr His Ala Lys Gly Leu Asp Ile Ala Thr Ala Ala Tyr Val Ala Glu
485 490 495

Ala Thr Pro Gly Pro Thr His Ile Gln Ser Ala Glu Met His Asn Gln
500 505 510

Ala Val Asn Ser Leu Ala Leu Ile Ser Ala Arg Ala Thr Ile Thr Ser
515 520 525

Leu Glu Val Leu Thr Ser Leu Ile Ala Ser Tyr Leu Tyr Ile Leu Cys
530 535 540

Gln Ala Leu Asp Leu Arg Ala Leu Gln Arg Glu Phe Leu Pro Gly Leu
545 550 555 560

Asp Ile Ile Ile Arg Glu Glu Leu Arg Ser Ser Phe Gly Ser Phe Leu
565 570 575

Ser Ser Glu Gln Met Glu Lys Leu Gln Gln Asn Leu Thr Ser Ala Phe
580 585 590

Glu Asp His Leu Asp Lys Thr Thr Thr Met Asp Asn Thr Asp Arg Met
595 600 605

Thr Thr Met Ala Ala Thr Ser Ser Ser Val Leu Leu Gln Phe Phe Thr
610 615 620

Asp Ser Gly Ala Ser Val Pro Pro Ser Ser Cys Asp Leu Leu Ser Ser
625 630 635 640

Val Ser Ser Phe Gln Ser Ser Val Ala Thr Arg Ser Ser Val Leu Met
645 650 655

Asp Asp Leu Arg Lys Glu Tyr Ile Phe Gly Asp Arg Gly Pro Thr Pro
660 665 670

Ala Ser Gln Tyr Ile Gly Lys Thr Arg Pro Val Tyr Gln Phe Ile Arg
675 680 685

Thr Thr Ile Gly Val Arg Lys His Gly Ser Glu Asn Tyr Asn Lys Phe
690 695 700

Tyr Asn Gly Leu Gly Val Glu Asp Val Thr Ile Gly Gln Asn Ile Ser
705 710 715 720

Arg Ile Tyr Glu Ser Ile Arg Asp Gly Lys Met Gln Ser Ile Ile Val
725 730 735

Ser Leu Phe Asp
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<222> (646)..(2784)

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tcggcttgtt cctctcctct ataqacatgg gtactgatca cttcgtttgt tgttctcgtt 180

ttctcttgca agtacgaccc atccttttttt ctcgcgatcg acttcaatat cggtgcgctt 240

gcactacgtc tcttcgccag tgcacagtat gacgggaggg gacacgactg gcggcgaaag 300

cggagtcgtc gttgccggtc ccgagagacg ggaacacttt cttccgcctt ccagaggccg 360

tactccggtg atttgacatc gcactatgct tggtggggcg cccgaactcg gagcttgcga 420

tgtgcctgaa gcagagctcg gcaggcgaca tggcgactcc gccacattcg ggtcaaagcc 480

gaagtggggc ctcggacgtt ccgaacgtcg tcttgccgcc gccgcgttgc gtccgccgtc 540

gactttgtcc tcgtgtgctc acgcctcctt ctttctctct tctgctttcc tcacttcact 600

ctgcaagtcc cgcctcgcat ccacccaacc cgagcagctc tcaag atg gcc ccc tcc 657
Met Ala Pro Ser
1

gtc gac tcg atc gcg act tcg gtt gcc aac tcc ctc tcg aac ggg ttg 705
Val Asp Ser Ile Ala Thr Ser Val Ala Asn Ser Leu Ser Asn Gly Leu
5 10 15 20

```
cac gcc gcc gcc gcc gcc aac ggt ggc gac gtc cac aag aag acg gcc   753
His Ala Ala Ala Ala Ala Asn Gly Gly Asp Val His Lys Lys Thr Ala
                 25                  30                  35

ggt gct ggc tcc ctc ctc ccg acc acc gag acg acc cag ctc gac atc   801
Gly Ala Gly Ser Leu Leu Pro Thr Thr Glu Thr Thr Gln Leu Asp Ile
             40                  45                  50

gtt gag cgc atc ttg gcc gac gcc ggc gcg acg gac cag atc aaa ctc   849
Val Glu Arg Ile Leu Ala Asp Ala Gly Ala Thr Asp Gln Ile Lys Leu
         55                  60                  65

gat ggg tac acc ctc acg ctc ggc gac gtc gtc ggc gct gct cgc cgt   897
Asp Gly Tyr Thr Leu Thr Leu Gly Asp Val Val Gly Ala Ala Arg Arg
     70                  75                  80

ggc cgc tcc gtc aag gtc gca gac agc ccg cac atc cgc gag aag atc   945
Gly Arg Ser Val Lys Val Ala Asp Ser Pro His Ile Arg Glu Lys Ile
 85                  90                  95                 100

gat gcc agt gtc gag ttc ctc cgt act cag ctc gac aac agt gtc tac   993
Asp Ala Ser Val Glu Phe Leu Arg Thr Gln Leu Asp Asn Ser Val Tyr
                105                 110                 115

ggt gtc acg act ggt ttc ggc ggc tcg gcc gac acc cgg act gag gat   1041
Gly Val Thr Thr Gly Phe Gly Gly Ser Ala Asp Thr Arg Thr Glu Asp
            120                 125                 130

gcg atc tcg ctc caa aag gcc ctg ctc gag cac cag ctc tgc ggt gtc   1089
Ala Ile Ser Leu Gln Lys Ala Leu Leu Glu His Gln Leu Cys Gly Val
        135                 140                 145

ctc ccc acc tcg atg gat ggc ttt gcg ctc ggt cgc ggc ctc gag aac   1137
Leu Pro Thr Ser Met Asp Gly Phe Ala Leu Gly Arg Gly Leu Glu Asn
    150                 155                 160

tcg ctt ccg ctc gaa gtc gtc cga ggc gcg atg acc atc cgt gtc aac   1185
Ser Leu Pro Leu Glu Val Val Arg Gly Ala Met Thr Ile Arg Val Asn
165                 170                 175                 180

tcg ctc act cgc ggt cac tcg gcg gtc cgc atc gtc gtc ctc gaa gcc   1233
Ser Leu Thr Arg Gly His Ser Ala Val Arg Ile Val Val Leu Glu Ala
                185                 190                 195

ctc acc aac ttc ctc aac cac ggc atc acc ccg atc gtc ccg ctt cga   1281
Leu Thr Asn Phe Leu Asn His Gly Ile Thr Pro Ile Val Pro Leu Arg
            200                 205                 210
```

```
ggc acc atc tcg gcg tcg ggc gac ctt tcc ccc ctc tct tac atc gcc   1329
Gly Thr Ile Ser Ala Ser Gly Asp Leu Ser Pro Leu Ser Tyr Ile Ala
        215                 220                 225

gcc tcg atc acc ggc cac ccg gac tcg aag gtc cac gtc gac ggc aag   1377
Ala Ser Ile Thr Gly His Pro Asp Ser Lys Val His Val Asp Gly Lys
    230                 235                 240

atc atg tcc gcc cag gag gcg atc gcg ctc aag ggt ctt cag ccc gtc   1425
Ile Met Ser Ala Gln Glu Ala Ile Ala Leu Lys Gly Leu Gln Pro Val
245                 250                 255                 260

gtc ctc ggt ccg aag gag ggt ctc ggt ctc gtc aac ggc acg gcc gtc   1473
Val Leu Gly Pro Lys Glu Gly Leu Gly Leu Val Asn Gly Thr Ala Val
                265                 270                 275

tcc gcc tcg atg gcg acg ctg gcc ctc acc gac gca cac gtc ctc tcg   1521
Ser Ala Ser Met Ala Thr Leu Ala Leu Thr Asp Ala His Val Leu Ser
            280                 285                 290

ctc ctc gca cag gcg ctc act gct ctt act gtc gag gcc atg gtc gga   1569
Leu Leu Ala Gln Ala Leu Thr Ala Leu Thr Val Glu Ala Met Val Gly
        295                 300                 305

cac gcc ggc tcg ttc cac cca ttc ctc cac gac gtc acg cgc cct cac   1617
His Ala Gly Ser Phe His Pro Phe Leu His Asp Val Thr Arg Pro His
    310                 315                 320

ccg acc cag atc gag gtg gcg cgc aac atc cgg act ctt ctc gag ggc   1665
Pro Thr Gln Ile Glu Val Ala Arg Asn Ile Arg Thr Leu Leu Glu Gly
325                 330                 335                 340

agc aag tac gcc gtc cac cac gag act gaa gtc aag gtc aag gac gac   1713
Ser Lys Tyr Ala Val His His Glu Thr Glu Val Lys Val Lys Asp Asp
                345                 350                 355

gag ggc atc ctc agg cag gac cgg tac ccg ctc cgc tgc tcg ccg cag   1761
Glu Gly Ile Leu Arg Gln Asp Arg Tyr Pro Leu Arg Cys Ser Pro Gln
            360                 365                 370

tgg ctc ggt ccc ctt gtc agc gac atg att cac gct cac gct gtc ctc   1809
Trp Leu Gly Pro Leu Val Ser Asp Met Ile His Ala His Ala Val Leu
        375                 380                 385

tcg ctc gag gct ggt cag tcg acc acc gac aac ccg ctg atc gac ctc   1857
Ser Leu Glu Ala Gly Gln Ser Thr Thr Asp Asn Pro Leu Ile Asp Leu
    390                 395                 400
```

```
gag aac aag atg acc cac cat ggc gga gcc ttc atg gcg agc agc gtc   1905
Glu Asn Lys Met Thr His His Gly Gly Ala Phe Met Ala Ser Ser Val
405                 410                 415                 420

gga aac acg atg gag aag act cgc ctc gcc gtc gcg ctg atg ggc aag   1953
Gly Asn Thr Met Glu Lys Thr Arg Leu Ala Val Ala Leu Met Gly Lys
                425                 430                 435

gtc agc ttt act cag ctc acc gag atg ctc aac gcc ggc atg aac cgg   2001
Val Ser Phe Thr Gln Leu Thr Glu Met Leu Asn Ala Gly Met Asn Arg
            440                 445                 450

gcc ctt ccg tcc tgc ctc gct gcc gag gac cct tcc ctc tct tat cac   2049
Ala Leu Pro Ser Cys Leu Ala Ala Glu Asp Pro Ser Leu Ser Tyr His
        455                 460                 465

tgc aag ggt ctc gac att gct gcg gcc gcc tac act tcc gag ctc ggt   2097
Cys Lys Gly Leu Asp Ile Ala Ala Ala Ala Tyr Thr Ser Glu Leu Gly
    470                 475                 480

cac ctt gcc aac ccg gtt tcg acc cac gtc cag ccg gcc gag atg ggc   2145
His Leu Ala Asn Pro Val Ser Thr His Val Gln Pro Ala Glu Met Gly
485                 490                 495                 500

aac cag gcc atc aac tcg ctc gcc ctc atc tcg gcc cgc cgc acc gcc   2193
Asn Gln Ala Ile Asn Ser Leu Ala Leu Ile Ser Ala Arg Arg Thr Ala
                505                 510                 515

gag gcg aac gac gtt ctc tcc ctc ctc ctc gcc acc cac ctc tac tgc   2241
Glu Ala Asn Asp Val Leu Ser Leu Leu Leu Ala Thr His Leu Tyr Cys
            520                 525                 530

gtc ctc cag gcc gtc gac ctc cgc gcg atg gag ttt gag cac acc aag   2289
Val Leu Gln Ala Val Asp Leu Arg Ala Met Glu Phe Glu His Thr Lys
        535                 540                 545

gcg ttc gag ccg atg gtc act gag ctg ttg aag cag cac ttt ggc gcg   2337
Ala Phe Glu Pro Met Val Thr Glu Leu Leu Lys Gln His Phe Gly Ala
    550                 555                 560

ctc gcg acg gcc gaa gtc gag gac aag gtc cgc aag tcg atc tac aag   2385
Leu Ala Thr Ala Glu Val Glu Asp Lys Val Arg Lys Ser Ile Tyr Lys
565                 570                 575                 580

cgg ttg cag cag aac aac tcg tac gac ctc gag cag cgg tgg cac gac   2433
Arg Leu Gln Gln Asn Asn Ser Tyr Asp Leu Glu Gln Arg Trp His Asp
                585                 590                 595
```

```
acg ttc tcg gtc gcg acc ggt gcc gtc gtc gag gcg ctc gcc ggc cag   2481
Thr Phe Ser Val Ala Thr Gly Ala Val Val Glu Ala Leu Ala Gly Gln
            600                 605                 610

gag gtc tcg ctc gcg agc ctc aac gcc tgg aag gtc gcc tgc gcc gag   2529
Glu Val Ser Leu Ala Ser Leu Asn Ala Trp Lys Val Ala Cys Ala Glu
        615                 620                 625

aag gct atc gcg ctc acg cgc tcc gtc cgc gac tcg ttc tgg gcg gct   2577
Lys Ala Ile Ala Leu Thr Arg Ser Val Arg Asp Ser Phe Trp Ala Ala
    630                 635                 640

ccg tcg tcg tcg tcg ccc gcg ctc aag tac ctc tcc ccg cgg acg cgc   2625
Pro Ser Ser Ser Ser Pro Ala Leu Lys Tyr Leu Ser Pro Arg Thr Arg
645                 650                 655                 660

gtc ctg tat tcg ttc gtc cgg gag gag gtc ggc gtc aag gcc cgc cgc   2673
Val Leu Tyr Ser Phe Val Arg Glu Glu Val Gly Val Lys Ala Arg Arg
                665                 670                 675

ggc gat gtc tac ctc ggc aag cag gag gtc acg atc ggc acc aac gtc   2721
Gly Asp Val Tyr Leu Gly Lys Gln Glu Val Thr Ile Gly Thr Asn Val
            680                 685                 690

agc cgc atc tac gag gcg atc aag agc ggt tgc atc gcc ccc gtc ctc   2769
Ser Arg Ile Tyr Glu Ala Ile Lys Ser Gly Cys Ile Ala Pro Val Leu
        695                 700                 705

gtc aag atg atg gca tag                                          2787
Val Lys Met Met Ala
    710
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<210> 17
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<213> Rhodotorula mucilaginosa

<400> 17

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Met Ala Pro Ser Val Asp Ser Ile Ala Thr Ser Val Ala Asn Ser Leu
  1               5                  10                  15

Ser Asn Gly Leu His Ala Ala Ala Ala Ala Asn Gly Gly Asp Val His
             20                  25                  30

Lys Lys Thr Ala Gly Ala Gly Ser Leu Leu Pro Thr Thr Glu Thr Thr
         35                  40                  45
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Gln Leu Asp Ile Val Glu Arg Ile Leu Ala Asp Ala Gly Ala Thr Asp
50 55 60

Gln Ile Lys Leu Asp Gly Tyr Thr Leu Thr Leu Gly Asp Val Val Gly
65 70 75 80

Ala Ala Arg Arg Gly Arg Ser Val Lys Val Ala Asp Ser Pro His Ile
85 90 95

Arg Glu Lys Ile Asp Ala Ser Val Glu Phe Leu Arg Thr Gln Leu Asp
100 105 110

Asn Ser Val Tyr Gly Val Thr Thr Gly Phe Gly Gly Ser Ala Asp Thr
115 120 125

Arg Thr Glu Asp Ala Ile Ser Leu Gln Lys Ala Leu Leu Glu His Gln
130 135 140

Leu Cys Gly Val Leu Pro Thr Ser Met Asp Gly Phe Ala Leu Gly Arg
145 150 155 160

Gly Leu Glu Asn Ser Leu Pro Leu Glu Val Val Arg Gly Ala Met Thr
165 170 175

Ile Arg Val Asn Ser Leu Thr Arg Gly His Ser Ala Val Arg Ile Val
180 185 190

Val Leu Glu Ala Leu Thr Asn Phe Leu Asn His Gly Ile Thr Pro Ile
195 200 205

Val Pro Leu Arg Gly Thr Ile Ser Ala Ser Gly Asp Leu Ser Pro Leu
210 215 220

Ser Tyr Ile Ala Ala Ser Ile Thr Gly His Pro Asp Ser Lys Val His
225 230 235 240

Val Asp Gly Lys Ile Met Ser Ala Gln Glu Ala Ile Ala Leu Lys Gly
245 250 255

Leu Gln Pro Val Val Leu Gly Pro Lys Glu Gly Leu Gly Leu Val Asn
260 265 270

Gly Thr Ala Val Ser Ala Ser Met Ala Thr Leu Ala Leu Thr Asp Ala
275 280 285

His Val Leu Ser Leu Leu Ala Gln Ala Leu Thr Ala Leu Thr Val Glu
290 295 300

Ala Met Val Gly His Ala Gly Ser Phe His Pro Phe Leu His Asp Val
305 310 315 320

Thr Arg Pro His Pro Thr Gln Ile Glu Val Ala Arg Asn Ile Arg Thr
325 330 335

Leu Leu Glu Gly Ser Lys Tyr Ala Val His His Glu Thr Glu Val Lys
340 345 350

Val Lys Asp Asp Glu Gly Ile Leu Arg Gln Asp Arg Tyr Pro Leu Arg
355 360 365

Cys Ser Pro Gln Trp Leu Gly Pro Leu Val Ser Asp Met Ile His Ala
370 375 380

His Ala Val Leu Ser Leu Glu Ala Gly Gln Ser Thr Thr Asp Asn Pro
385 390 395 400

Leu Ile Asp Leu Glu Asn Lys Met Thr His His Gly Gly Ala Phe Met
405 410 415

Ala Ser Ser Val Gly Asn Thr Met Glu Lys Thr Arg Leu Ala Val Ala
420 425 430

Leu Met Gly Lys Val Ser Phe Thr Gln Leu Thr Glu Met Leu Asn Ala
435 440 445

Gly Met Asn Arg Ala Leu Pro Ser Cys Leu Ala Ala Glu Asp Pro Ser
450 455 460

Leu Ser Tyr His Cys Lys Gly Leu Asp Ile Ala Ala Ala Ala Tyr Thr
465 470 475 480

Ser Glu Leu Gly His Leu Ala Asn Pro Val Ser Thr His Val Gln Pro
485 490 495

Ala Glu Met Gly Asn Gln Ala Ile Asn Ser Leu Ala Leu Ile Ser Ala
500 505 510

Arg Arg Thr Ala Glu Ala Asn Asp Val Leu Ser Leu Leu Leu Ala Thr
515 520 525

His Leu Tyr Cys Val Leu Gln Ala Val Asp Leu Arg Ala Met Glu Phe
530 535 540

Glu His Thr Lys Ala Phe Glu Pro Met Val Thr Glu Leu Leu Lys Gln
545 550 555 560

```
His Phe Gly Ala Leu Ala Thr Ala Glu Val Glu Asp Lys Val Arg Lys
                565                 570                 575

Ser Ile Tyr Lys Arg Leu Gln Gln Asn Asn Ser Tyr Asp Leu Glu Gln
            580                 585                 590

Arg Trp His Asp Thr Phe Ser Val Ala Thr Gly Ala Val Val Glu Ala
        595                 600                 605

Leu Ala Gly Gln Glu Val Ser Leu Ala Ser Leu Asn Ala Trp Lys Val
    610                 615                 620

Ala Cys Ala Glu Lys Ala Ile Ala Leu Thr Arg Ser Val Arg Asp Ser
625                 630                 635                 640

Phe Trp Ala Ala Pro Ser Ser Ser Ser Pro Ala Leu Lys Tyr Leu Ser
                645                 650                 655

Pro Arg Thr Arg Val Leu Tyr Ser Phe Val Arg Glu Glu Val Gly Val
            660                 665                 670

Lys Ala Arg Arg Gly Asp Val Tyr Leu Gly Lys Gln Glu Val Thr Ile
        675                 680                 685

Gly Thr Asn Val Ser Arg Ile Tyr Glu Ala Ile Lys Ser Gly Cys Ile
    690                 695                 700

Ala Pro Val Leu Val Lys Met Met Ala
705                 710
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<210> 18
<211> 2439
<212> DNA
<213> Rhodotorula toruloides

<220>
<221> CDS
<222> (1)..(2148)

<400> 18

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Met Ala Pro Ser Leu Asp Ser Ile Ser His Ser Phe Ala Asn Gly Val
  1               5                  10                  15

gca tcc gca aag cag gct gtc aat ggc gcc tcg acc aac ctc gca gtc   96
Ala Ser Ala Lys Gln Ala Val Asn Gly Ala Ser Thr Asn Leu Ala Val
            20                  25                  30
```

```
gca ggc tcg cac ctg ccc aca acc cag gtc acg cag gtc gac atc gtc   144
Ala Gly Ser His Leu Pro Thr Thr Gln Val Thr Gln Val Asp Ile Val
         35                  40                  45

gag aag atg ctc gcc gcg ccg acc gac tcg acg ctc gaa ctc gac ggc   192
Glu Lys Met Leu Ala Ala Pro Thr Asp Ser Thr Leu Glu Leu Asp Gly
     50                  55                  60

tac tcg ctc aac ctc gga gac gtc gtc tcg gcc gcg agg aag ggc agg   240
Tyr Ser Leu Asn Leu Gly Asp Val Val Ser Ala Ala Arg Lys Gly Arg
 65                  70                  75                  80

cct gtc cgc gtc aag gac agc gac gag atc cgc tca aag att gac aaa   288
Pro Val Arg Val Lys Asp Ser Asp Glu Ile Arg Ser Lys Ile Asp Lys
                 85                  90                  95

tcg gtc gag ttc ttg cgc tcg caa ctc tcc atg agc gtc tac ggc gtc   336
Ser Val Glu Phe Leu Arg Ser Gln Leu Ser Met Ser Val Tyr Gly Val
            100                 105                 110

acg act gga ttt ggc gga tcc gca gac acc cgc acc gag gac gcc atc   384
Thr Thr Gly Phe Gly Gly Ser Ala Asp Thr Arg Thr Glu Asp Ala Ile
        115                 120                 125

tcg ctc cag aag gct ctc ctc gag cac cag ctc tgc ggt gtt ctc cct   432
Ser Leu Gln Lys Ala Leu Leu Glu His Gln Leu Cys Gly Val Leu Pro
    130                 135                 140

tcg tcg ttc gac tcg ttc cgc ctc ggc cgc ggt ctc gag aac tcg ctt   480
Ser Ser Phe Asp Ser Phe Arg Leu Gly Arg Gly Leu Glu Asn Ser Leu
145                 150                 155                 160

ccc ctc gag gtt gtt cgc ggc gcc atg aca atc cgc gtc aac agc ttg   528
Pro Leu Glu Val Val Arg Gly Ala Met Thr Ile Arg Val Asn Ser Leu
                165                 170                 175

acc cgc ggc cac tcg gct gtc cgc ctc gtc gtc ctc gag gcg ctc acc   576
Thr Arg Gly His Ser Ala Val Arg Leu Val Val Leu Glu Ala Leu Thr
            180                 185                 190

aac ttc ctc aac cac ggc atc acc ccc atc gtc ccc ctc cgc ggc acc   624
Asn Phe Leu Asn His Gly Ile Thr Pro Ile Val Pro Leu Arg Gly Thr
        195                 200                 205

atc tct gcg tcg ggc gac ctc tct cct ctc tcc tac att gca gcg gcc   672
Ile Ser Ala Ser Gly Asp Leu Ser Pro Leu Ser Tyr Ile Ala Ala Ala
    210                 215                 220
```

```
atc agc ggt cac ccg gac agc aag gtg cac gtc gtc cac gag ggc aag   720
Ile Ser Gly His Pro Asp Ser Lys Val His Val Val His Glu Gly Lys
225                 230                 235                 240

gag aag atc ctg tac gcc cgc gag gcg atg gcg ctc ttc aac ctc gag   768
Glu Lys Ile Leu Tyr Ala Arg Glu Ala Met Ala Leu Phe Asn Leu Glu
                245                 250                 255

ccc gtc gtc ctc ggc ccg aag gaa ggt ctc ggt ctc gtc aac ggc acc   816
Pro Val Val Leu Gly Pro Lys Glu Gly Leu Gly Leu Val Asn Gly Thr
            260                 265                 270

gcc gtc tca gca tcg atg gcc acc ctc gct ctg cac gac gca cac atg   864
Ala Val Ser Ala Ser Met Ala Thr Leu Ala Leu His Asp Ala His Met
        275                 280                 285

ctc tcg ctc ctc tcg cag tcg ctc acg gcc atg acg gtc gaa gcg atg   912
Leu Ser Leu Leu Ser Gln Ser Leu Thr Ala Met Thr Val Glu Ala Met
    290                 295                 300

gtc ggc cac gcc ggc tcg ttc cac ccc ttc ctt cac gac gtc acg cgc   960
Val Gly His Ala Gly Ser Phe His Pro Phe Leu His Asp Val Thr Arg
305                 310                 315                 320

cct cac ccg acg cag atc gaa gtc gcg gga aac atc cgc aag ctc ctc  1008
Pro His Pro Thr Gln Ile Glu Val Ala Gly Asn Ile Arg Lys Leu Leu
                325                 330                 335

gag gga agc cgc ttt gct gtc cac cat gag gag gag gtc aag gtc aag  1056
Glu Gly Ser Arg Phe Ala Val His His Glu Glu Glu Val Lys Val Lys
            340                 345                 350

gac gac gag ggc att ctc cgc cag gac cgc tac ccc ttg cgc acg tct  1104
Asp Asp Glu Gly Ile Leu Arg Gln Asp Arg Tyr Pro Leu Arg Thr Ser
        355                 360                 365

cct cag tgg ctc ggc ccg ctc gtc agc gac ctc att cac gcc cac gcc  1152
Pro Gln Trp Leu Gly Pro Leu Val Ser Asp Leu Ile His Ala His Ala
    370                 375                 380

gtc ctc acc atc gag gcc ggc cag tcg acg acc gac aac cct ctc atc  1200
Val Leu Thr Ile Glu Ala Gly Gln Ser Thr Thr Asp Asn Pro Leu Ile
385                 390                 395                 400

gac gtc gag aac aag act tcg cac cac ggc ggc aat ttc cag gct gcc  1248
Asp Val Glu Asn Lys Thr Ser His His Gly Gly Asn Phe Gln Ala Ala
                405                 410                 415
```

```
gct gtg gcc aac acc atg gag aag act cgc ctc ggg ctc gcc cag atc   1296
Ala Val Ala Asn Thr Met Glu Lys Thr Arg Leu Gly Leu Ala Gln Ile
            420                 425                 430

ggc aag ctc aac ttc acg cag ctc acc gag atg ctc aac gcc ggc atg   1344
Gly Lys Leu Asn Phe Thr Gln Leu Thr Glu Met Leu Asn Ala Gly Met
        435                 440                 445

aac cgc ggc ctc ccc tcc tgc ctc gcg gcc gaa gac ccc tcg ctc tcc   1392
Asn Arg Gly Leu Pro Ser Cys Leu Ala Ala Glu Asp Pro Ser Leu Ser
    450                 455                 460

tac cac tgc aag ggc ctc gac atc gcc gct gcg gcg tac acc tcg gag   1440
Tyr His Cys Lys Gly Leu Asp Ile Ala Ala Ala Ala Tyr Thr Ser Glu
465                 470                 475                 480

ttg gga cac ctc gcc aac cct gtg acg acg cat gtc cag ccg gct gag   1488
Leu Gly His Leu Ala Asn Pro Val Thr Thr His Val Gln Pro Ala Glu
                485                 490                 495

atg gcg aac cag gcg gtc aac tcg ctt gcg ctc atc tcg gct cgt cgc   1536
Met Ala Asn Gln Ala Val Asn Ser Leu Ala Leu Ile Ser Ala Arg Arg
            500                 505                 510

acg acc gag tcc aac gac gtc ctt tct ctc ctc ctc gcc acc cac ctc   1584
Thr Thr Glu Ser Asn Asp Val Leu Ser Leu Leu Leu Ala Thr His Leu
        515                 520                 525

tac tgc gtt ctc caa gcc atc gac ttg cgc gcg atc gag ttc gag ttc   1632
Tyr Cys Val Leu Gln Ala Ile Asp Leu Arg Ala Ile Glu Phe Glu Phe
    530                 535                 540

aag aag cag ttc ggc cca gcc atc gtc tcg ctc atc gac cag cac ttt   1680
Lys Lys Gln Phe Gly Pro Ala Ile Val Ser Leu Ile Asp Gln His Phe
545                 550                 555                 560

ggc tcc gcc atg acc ggc tcg aac ctg cgc gac gag ctc gtc gag aag   1728
Gly Ser Ala Met Thr Gly Ser Asn Leu Arg Asp Glu Leu Val Glu Lys
                565                 570                 575

gtg aac aag acg ctc gcc aag cgc ctc gag cag acc aac tcg tac gac   1776
Val Asn Lys Thr Leu Ala Lys Arg Leu Glu Gln Thr Asn Ser Tyr Asp
            580                 585                 590

ctc gtc ccg cgc tgg cac gac gcc ttc tcc ttc gcc gcc ggc acc gtc   1824
Leu Val Pro Arg Trp His Asp Ala Phe Ser Phe Ala Ala Gly Thr Val
        595                 600                 605
```

```
gtc gag gtc ctc tcg tcg acg tcg ctc tcg ctc gcc gcc gtc aac gcc   1872
Val Glu Val Leu Ser Ser Thr Ser Leu Ser Leu Ala Ala Val Asn Ala
    610                 615                 620

tgg aag gtc gcc gcc gcc gag tcg gcc atc tcg ctc acc cgc caa gtc   1920
Trp Lys Val Ala Ala Ala Glu Ser Ala Ile Ser Leu Thr Arg Gln Val
625                 630                 635                 640

cgc gag acc ttc tgg tcc gcc gcg tcg acc tcg tcg ccc gcg ctc tcg   1968
Arg Glu Thr Phe Trp Ser Ala Ala Ser Thr Ser Ser Pro Ala Leu Ser
                645                 650                 655

tac ctc tcg ccg cgc act cag atc ctc tac gcc ttc gtc cgc gag gag   2016
Tyr Leu Ser Pro Arg Thr Gln Ile Leu Tyr Ala Phe Val Arg Glu Glu
            660                 665                 670

ctt ggc gtc aag gcc cgc cgc gga gac gtc ttc ctc ggc aag caa gag   2064
Leu Gly Val Lys Ala Arg Arg Gly Asp Val Phe Leu Gly Lys Gln Glu
        675                 680                 685

gtg acg atc ggc tcg aac gtc tcc aag atc tac gag gcc atc aag tcg   2112
Val Thr Ile Gly Ser Asn Val Ser Lys Ile Tyr Glu Ala Ile Lys Ser
    690                 695                 700

ggc agg atc aac aac gtc ctc ctc aag atg ctc gct tagacactct        2158
Gly Arg Ile Asn Asn Val Leu Leu Lys Met Leu Ala
705                 710                 715

tcccactctc gcatcccttc cataccctat cccgcctgca ctcttaggac tcgcttcttg 2218

tcggactcgg atctcgcatc gcttctttcg ttcttggctg cctctctaga ccgtgtccgt 2278

attacctcga gattgtgaat acaagcagta cccatccacg catccgataa atcagggaga 2338

gaatctacgc ttgcgggagc ttcttgcgca taaactgtcg agtgcgggcg ttagtgcgaa 2398

gtcaacgaag gcgagtggca gcggctcact accgcctcga g                     2439
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<210> 19
<211> 716
<212> PRT
<213> Rhodotorula toruloides

<400> 19

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Met Ala Pro Ser Leu Asp Ser Ile Ser His Ser Phe Ala Asn Gly Val
  1               5                  10                  15
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Ala Ser Ala Lys Gln Ala Val Asn Gly Ala Ser Thr Asn Leu Ala Val
20 25 30

Ala Gly Ser His Leu Pro Thr Thr Gln Val Thr Gln Val Asp Ile Val
35 40 45

Glu Lys Met Leu Ala Ala Pro Thr Asp Ser Thr Leu Glu Leu Asp Gly
50 55 60

Tyr Ser Leu Asn Leu Gly Asp Val Val Ser Ala Ala Arg Lys Gly Arg
65 70 75 80

Pro Val Arg Val Lys Asp Ser Asp Glu Ile Arg Ser Lys Ile Asp Lys
85 90 95

Ser Val Glu Phe Leu Arg Ser Gln Leu Ser Met Ser Val Tyr Gly Val
100 105 110

Thr Thr Gly Phe Gly Gly Ser Ala Asp Thr Arg Thr Glu Asp Ala Ile
115 120 125

Ser Leu Gln Lys Ala Leu Leu Glu His Gln Leu Cys Gly Val Leu Pro
130 135 140

Ser Ser Phe Asp Ser Phe Arg Leu Gly Arg Gly Leu Glu Asn Ser Leu
145 150 155 160

Pro Leu Glu Val Val Arg Gly Ala Met Thr Ile Arg Val Asn Ser Leu
165 170 175

Thr Arg Gly His Ser Ala Val Arg Leu Val Val Leu Glu Ala Leu Thr
180 185 190

Asn Phe Leu Asn His Gly Ile Thr Pro Ile Val Pro Leu Arg Gly Thr
195 200 205

Ile Ser Ala Ser Gly Asp Leu Ser Pro Leu Ser Tyr Ile Ala Ala Ala
210 215 220

Ile Ser Gly His Pro Asp Ser Lys Val His Val Val His Glu Gly Lys
225 230 235 240

Glu Lys Ile Leu Tyr Ala Arg Glu Ala Met Ala Leu Phe Asn Leu Glu
245 250 255

Pro Val Val Leu Gly Pro Lys Glu Gly Leu Gly Leu Val Asn Gly Thr
260 265 270

Ala Val Ser Ala Ser Met Ala Thr Leu Ala Leu His Asp Ala His Met
275 280 285

Leu Ser Leu Leu Ser Gln Ser Leu Thr Ala Met Thr Val Glu Ala Met
290 295 300

Val Gly His Ala Gly Ser Phe His Pro Phe Leu His Asp Val Thr Arg
305 310 315 320

Pro His Pro Thr Gln Ile Glu Val Ala Gly Asn Ile Arg Lys Leu Leu
325 330 335

Glu Gly Ser Arg Phe Ala Val His His Glu Glu Glu Val Lys Val Lys
340 345 350

Asp Asp Glu Gly Ile Leu Arg Gln Asp Arg Tyr Pro Leu Arg Thr Ser
355 360 365

Pro Gln Trp Leu Gly Pro Leu Val Ser Asp Leu Ile His Ala His Ala
370 375 380

Val Leu Thr Ile Glu Ala Gly Gln Ser Thr Thr Asp Asn Pro Leu Ile
385 390 395 400

Asp Val Glu Asn Lys Thr Ser His His Gly Gly Asn Phe Gln Ala Ala
405 410 415

Ala Val Ala Asn Thr Met Glu Lys Thr Arg Leu Gly Leu Ala Gln Ile
420 425 430

Gly Lys Leu Asn Phe Thr Gln Leu Thr Glu Met Leu Asn Ala Gly Met
435 440 445

Asn Arg Gly Leu Pro Ser Cys Leu Ala Ala Glu Asp Pro Ser Leu Ser
450 455 460

Tyr His Cys Lys Gly Leu Asp Ile Ala Ala Ala Ala Tyr Thr Ser Glu
465 470 475 480

Leu Gly His Leu Ala Asn Pro Val Thr Thr His Val Gln Pro Ala Glu
485 490 495

Met Ala Asn Gln Ala Val Asn Ser Leu Ala Leu Ile Ser Ala Arg Arg
500 505 510

Thr Thr Glu Ser Asn Asp Val Leu Ser Leu Leu Leu Ala Thr His Leu
515 520 525

Tyr Cys Val Leu Gln Ala Ile Asp Leu Arg Ala Ile Glu Phe Glu Phe
530 535 540

Lys Lys Gln Phe Gly Pro Ala Ile Val Ser Leu Ile Asp Gln His Phe
545 550 555 560

Gly Ser Ala Met Thr Gly Ser Asn Leu Arg Asp Glu Leu Val Glu Lys
565 570 575

Val Asn Lys Thr Leu Ala Lys Arg Leu Glu Gln Thr Asn Ser Tyr Asp
580 585 590

Leu Val Pro Arg Trp His Asp Ala Phe Ser Phe Ala Ala Gly Thr Val
595 600 605

Val Glu Val Leu Ser Ser Thr Ser Leu Ser Leu Ala Ala Val Asn Ala
610 615 620

Trp Lys Val Ala Ala Ala Glu Ser Ala Ile Ser Leu Thr Arg Gln Val
625 630 635 640

Arg Glu Thr Phe Trp Ser Ala Ala Ser Thr Ser Ser Pro Ala Leu Ser
645 650 655

Tyr Leu Ser Pro Arg Thr Gln Ile Leu Tyr Ala Phe Val Arg Glu Glu
660 665 670

Leu Gly Val Lys Ala Arg Arg Gly Asp Val Phe Leu Gly Lys Gln Glu
675 680 685

Val Thr Ile Gly Ser Asn Val Ser Lys Ile Tyr Glu Ala Ile Lys Ser
690 695 700

Gly Arg Ile Asn Asn Val Leu Leu Lys Met Leu Ala
705 710 715

<210> 20
<211> 2475
<212> DNA
<213> Artificial Sequence

<220>
<221> misc_difference
<222> (13, 34, 46, 49, 51, 57, 59, 68, 69, 73, 75 - 77, 79, 82, 84,
102, 106, 108, 115, 119, 144, 145, 164, 168, 190, 191, 195, 199 -
201, 233, 251, 264, 266, 276, 284, 312, 315, 330, 331, 333, 340,
348, 357, 405, 423, 450, 456, 463, 468, 475, 483, 555, 570, 675,
681, 715, 716, 723, 729, 730, 732, 743, 744, 758, 783, 921, 963,

1042, 1043, 1176, 1197, 1241, 1270, 1281, 1308, 1380, 1383, 1407, 1446, 1449, 1452, 1470, 1488, 1509, 1542, 1554, 1563, 1617, 1675, 1677, 1678, 1681, 1683, 1684, 1690, 1693, 1708, 1710, 1723 - 1735, 1745, 1762, 1768, 1776, 1855 - 1862, 1872 - 1875, 1880, 1881, 1895, 1950, 1952, 1962, 1971, 1976, 2001, 2145, 2146, 2151, 2183, 2187 - 2189, 2191, 2193 - 2195, 2197, 2199, 2206, 2208 - 2212, 2215 - 2217, 2219, 2221 - 2223, 2226 - 2233, 2236, 2239, 2241 -2243, 2247, 2248, 2251, 2254, 2256 - 2260, 2265, 2266, 2268, 2269, 2271, 2272, 2274 - 2280, 2282 - 2285, 2287, 2289, 2290, 2293, 2294, 2298, 2300 - 2303, 2305, 2307, 2308, 2312, 2313, 2315 - 2319, 2322 - 2324, 2326, 2327, 2329 - 2335, 2337 - 2339, 2341, 2344 - 2346, 2349 - 2351, 2354, 2356, 2358 - 2363, 2365, 2366, 2368, 2371, 2373, 2374, 2377, 2379, 2380, 2382, 2384, 2385, 2387, 2390, 2392, 2393, 2395 - 2403, 2405, 2409 - 2475)

<223> n = A or C or G or T; "n" indicates no consensus at that position

<223> Description of Artificial Sequence: Consensus Sequence of SEQ ID NOs: 12, 16, and 18

<400> 20

atggcccccc ccntcgactc gatcgcgacc tcgntcgcca acggcntcnc naacggntng 60

cacgccgnnc cgncnnngnc gncnacgggc gccacgtcca cnctcngncg gccgncgcng 120

gctcgctcct cccgaccacc cagnngacgc agctcgacat cgtngagnag atcctcgccg 180

accccaccgn nacgnacgnn ntcgaactcg acgggtacac cctcaccctc ggngacgtcg 240

tcggcgccgc ncgcaagggc cgcncngtcc gcgtcncaga cagncgacga gatccgcgca 300

aagatcgaca anagngtcga gttcctccgn ncncagctcn acaacagngt ctacggngtc 360

acgactggtt tcggcggctc ggccgacacc cggactgagg atgcnatctc gctccagaag 420

gcnctcctcg agcaccagct ctgcggtgtn ctcccnacgt cgntcgantc cttcngcctc 480

ggncgcggcc tcgagaactc gcttccgctc gaggtcgtcc gcggcgccat gaccatccgc 540

gtcaactcgc tcacncgcgg ccactcggcn gtccgcctcg tcgtcctcga ggcgctcacc 600

aacttcctca accacggcat cacccccatc gtccccctcc gcggcaccat ctcggcgtcg 660

ggcgacctct ccccnctctc ntacatcgcc gccgccatca ccggtcaccc ggacnncaag 720

gtncacgtnn tncacgaggg canngagaag atcatgtncg cccgcgaggc gatcgcgctc 780

ttnggtctcg agcccgtcgt cctcggcccg aaggagggtc tcggtctcgt caacggcacg 840

gccgtctccg cctcgatggc gaccctcgct ctgcacgacg cacacatgct ctcgctcctc 900

tcgcaggcgc tcacggctct nacggtcgag gccatggtcg gccacgccgg ctcgttccac 960

ccnttcctcc acgacgtcac gcgccctcac ccgacccaga tcgaggtcgc gcgcaacatc 1020

cgcacgctcc tcgagggcag cnngtttgcc gtccaccacg aggaggaggt caaggtcaag 1080

gacgacgagg gcattctccg ccaggaccgc tacccgctcc gcacgtcgcc tcagtggctc 1140

ggcccgctcg tcagcgacat gattcacgcc cacgcngtcc tctcgctcga ggccggncag 1200

tcgacgaccg acaacccgct catcgacgtc gagaacaaga ngacccacca cggcggcaac 1260

ttccaggcgn ccgctgtcgc naacacgatg gagaagactc gcctcgcnct cgccctgatc 1320

ggcaagctca acttcacgca gctcaccgag atgctcaacg ccggcatgaa ccgcggcctn 1380

ccntcctgcc tcgctgccga ggacccntcg ctctcctatc actgcaaggg cctcgacatt 1440

gccgcngcng cntacacttc ggagctcggn caccttgcca acccggtnac gacccacgtc 1500

cagccggcng agatgggcaa ccaggccgtc aactcgctcg cnctcatctc ggcncgccgc 1560

acngccgagg ccaacgacgt cctttctctc ctcctcgcca cccacctcta ctgcgtnctc 1620

caggccgtcg acctccgcgc gatggagttc gagttcaaga agcagttcga cccgntnntc 1680

ncnncgctcn tcnagcagca ctttggcncn gccctcgacg gcnnnnnnnn nnnnnacgaa 1740

ctcgnggaca aggtcaacaa gncgctcnac aagcgnctcg agcagaccaa ctcgtacgac 1800

ctcgagccgc gctggcacga cgccttctcg ttcgcgaccg gcaccgtcgt cgagnnnnnn 1860

nngtcctcgc cnnnngccan naggtctcgc tcgcngccgt caacgcctgg aaggtcgcct 1920

ccgccgagaa ggccatctcg ctcacgcgcn angtccgcga cnccttctgg ncggcnccgt 1980

cgtcgtcgtc gcccgcgctc ncgtacctct cgccgcgcac gcgcgtcctg tactcgttcg 2040

tccgcgagga gctcggcgtc aaggcccgcc gcggcgacgt cttcctcggc aagcaggagg 2100

tgacgatcgg caccaacgtc tcccgcatct acgaggccat caagnncggc ngcatcaacc 2160

acgtcctcgt caagatgctc gcntagnnnc ncnnncnann ctcgcntnnn nnccnnncnc 2220

nnnccnnnnn nnnctnttng nnntcgnntc ntgncnnnnn cgganntnnc nncnnnnnnn 2280

tnnnncntnn ctnnctcncn nnnancnngt cnntnnnnnc tnnngnntnn nnnnncnnnc 2340

ngtnnncann nacncntnnn nnnanncngg nanngantnn angnntncgn gnncnnnnnn 2400

nnnanaaann nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn 2460

nnnnnnnnnn nnnnn 2475

<210> 21
<211> 726
<212> PRT
<213> Artificial Sequence

<220>
<221> SITE
<222> (12, 16, 17, 20, 24, 25, 28 - 36, 38, 42, 47, 48, 56, 57, 62, 66, 67, 88, 92, 99, 110, 113, 154, 158, 243, 247, 252, 347, 413, 426, 556, 558 - 561, 564, 569 - 571, 573 - 578, 581, 582, 585, 587, 589, 610, 618, 622 - 626, 639, 649, 652, 653, 656, 666, 719)
<223> "Xaa" means any amino acid; "Xaa" means no consensus at that position

<223> Description of Artificial Sequence: Consensus of SEQ ID NOs: 13, 17, and 19

<400> 21

Met Ala Pro Ser Leu Asp Ser Ile Ala Thr Ser Xaa Ala Asn Gly Xaa
1 5 10 15

Xaa Asn Gly Xaa His Ala Ala Xaa Xaa Ala Ser Xaa Xaa Xaa Xaa Xaa
20 25 30

Xaa Xaa Xaa Xaa Ala Xaa Ala Gly Ser Xaa Leu Pro Thr Thr Xaa Xaa
35 40 45

Thr Gln Leu Asp Ile Val Glu Xaa Xaa Leu Ala Asp Pro Xaa Thr Asp
50 55 60

Asp Xaa Xaa Glu Leu Asp Gly Tyr Ser Leu Thr Leu Gly Asp Val Val
65 70 75 80

Gly Ala Ala Arg Lys Gly Arg Xaa Val Arg Val Xaa Asp Ser Asp Glu
85 90 95

Ile Arg Xaa Lys Ile Asp Lys Ser Val Glu Phe Leu Arg Xaa Gln Leu
100 105 110

Xaa Asn Ser Val Tyr Gly Val Thr Thr Gly Phe Gly Gly Ser Ala Asp
115 120 125

Thr Arg Thr Glu Asp Ala Ile Ser Leu Gln Lys Ala Leu Leu Glu His
130 135 140

Gln Leu Cys Gly Val Leu Pro Thr Ser Xaa Asp Ser Phe Xaa Leu Gly
145 150 155 160

Arg Gly Leu Glu Asn Ser Leu Pro Leu Glu Val Val Arg Gly Ala Met
165 170 175

Thr Ile Arg Val Asn Ser Leu Thr Arg Gly His Ser Ala Val Arg Leu
180 185 190

Val Val Leu Glu Ala Leu Thr Asn Phe Leu Asn His Gly Ile Thr Pro
195 200 205

Ile Val Pro Leu Arg Gly Thr Ile Ser Ala Ser Gly Asp Leu Ser Pro
210 215 220

Leu Ser Tyr Ile Ala Ala Ala Ile Thr Gly His Pro Asp Ser Lys Val
225 230 235 240

His Val Xaa His Glu Gly Xaa Glu Lys Ile Met Xaa Ala Arg Glu Ala
245 250 255

Ile Ala Leu Phe Gly Leu Glu Pro Val Val Leu Gly Pro Lys Glu Gly
260 265 270

Leu Gly Leu Val Asn Gly Thr Ala Val Ser Ala Ser Met Ala Thr Leu
275 280 285

Ala Leu His Asp Ala His Met Leu Ser Leu Leu Ser Gln Ala Leu Thr
290 295 300

Ala Leu Thr Val Glu Ala Met Val Gly His Ala Gly Ser Phe His Pro
305 310 315 320

Phe Leu His Asp Val Thr Arg Pro His Pro Thr Gln Ile Glu Val Ala
325 330 335

Arg Asn Ile Arg Thr Leu Leu Glu Gly Ser Xaa Phe Ala Val His His
340 345 350

Glu Glu Glu Val Lys Val Lys Asp Asp Glu Gly Ile Leu Arg Gln Asp
355 360 365

Arg Tyr Pro Leu Arg Thr Ser Pro Gln Trp Leu Gly Pro Leu Val Ser
370 375 380

Asp Met Ile His Ala His Ala Val Leu Ser Leu Glu Ala Gly Gln Ser
385 390 395 400

Thr Thr Asp Asn Pro Leu Ile Asp Val Glu Asn Lys Xaa Thr His His
405 410 415

Gly Gly Asn Phe Gln Ala Ser Ala Val Xaa Asn Thr Met Glu Lys Thr
420 425 430

Arg Leu Ala Leu Ala Leu Ile Gly Lys Leu Asn Phe Thr Gln Leu Thr
435 440 445

Glu Met Leu Asn Ala Gly Met Asn Arg Gly Leu Pro Ser Cys Leu Ala
450 455 460

Ala Glu Asp Pro Ser Leu Ser Tyr His Cys Lys Gly Leu Asp Ile Ala
465 470 475 480

Ala Ala Ala Tyr Thr Ser Glu Leu Gly His Leu Ala Asn Pro Val Thr
485 490 495

Thr His Val Gln Pro Ala Glu Met Gly Asn Gln Ala Val Asn Ser Leu
500 505 510

Ala Leu Ile Ser Ala Arg Arg Thr Ala Glu Ala Asn Asp Val Leu Ser
515 520 525

Leu Leu Leu Ala Thr His Leu Tyr Cys Val Leu Gln Ala Val Asp Leu
530 535 540

Arg Ala Met Glu Phe Glu Phe Lys Lys Gln Phe Xaa Pro Xaa Xaa Xaa
545 550 555 560

Xaa Leu Leu Xaa Gln His Phe Gly Xaa Xaa Xaa Thr Xaa Xaa Xaa Xaa
565 570 575

Xaa Xaa Glu Leu Xaa Xaa Lys Val Xaa Lys Xaa Leu Xaa Lys Arg Leu
580 585 590

Glu Gln Thr Asn Ser Tyr Asp Leu Glu Pro Arg Trp His Asp Ala Phe
595 600 605

Ser Xaa Ala Thr Gly Thr Val Val Glu Xaa Leu Ser Ser Xaa Xaa Xaa
610 615 620

Xaa Xaa Val Ser Leu Ala Ala Val Asn Ala Trp Lys Val Ala Xaa Ala
625 630 635 640

Glu Lys Ala Ile Ser Leu Thr Arg Xaa Val Arg Xaa Xaa Phe Trp Xaa
645 650 655

Ala Pro Ser Ser Ser Ser Pro Ala Leu Xaa Tyr Leu Ser Pro Arg Thr
660 665 670

Arg Val Leu Tyr Ser Phe Val Arg Glu Glu Leu Gly Val Lys Ala Arg
675 680 685

Arg Gly Asp Val Phe Leu Gly Lys Gln Glu Val Thr Ile Gly Ser Asn
690 695 700

Val Ser Arg Ile Tyr Glu Ala Ile Lys Ser Gly Arg Ile Asn Xaa Val
705 710 715 720

Leu Val Lys Met Leu Ala
725

<210> 22
<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Primer OLI 74

<400> 22
atccatatgg ctccttcttt ggattctctt gctactacgc tcgccaacgg ctttacc 57

<210> 23
<211> 60
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Primer OLI 75

<400> 23
atcgcggccg catgcggatc ctcattacgc gagcatcttg acgaggacgt ggttgatgcg 60

<210> 24
<211> 37
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Primer OLI 105

<400> 24
agtgaattca tggccccttc cttggactcg ctcgcca 37

<210> 25
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Primer OLI 80

<400> 25
atcgcatgct cattacgcga gcatcttgac gaggacgtgg ttgatgcg 48

<210> 26
<211> 39
<212> DNA
<213> Artificial

<220>
<223> Description of Artificial Sequence: oli 89

<400> 26
taaaagatct ccaccatggc cccttccttg gactcgctc
39

<210> 27
<211> 36
<212> DNA
<213> Artificial

<220>
<223> Description of Artificial Sequence: oli 90

<400> 27
caagcggccg cagagacgcg ggatacgaaa gaactg
36

<210> 28
<211> 2741
<212> DNA
<213> Rhodotorula graminis

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<222> (6)
<223> Description of modified_base: m = a or c

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<222> (1296)..(1364)
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<221> Intron
<222> (362)..(448)
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<400> 28

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atg gcm cct tcc ttg gac tcg ctc gcc acc acg ctc gcc aac ggc ttt      48
Met Ala Pro Ser Leu Asp Ser Leu Ala Thr Thr Leu Ala Asn Gly Phe
1               5                   10                  15

acc aac ggc tcg cac gcc gct ccg acc aag tcg gct gcg ggc ccc act      96
Thr Asn Gly Ser His Ala Ala Pro Thr Lys Ser Ala Ala Gly Pro Thr
            20                  25                  30

tcg gct ctc cgc cgc acg ccc ggc ctc gat ggc cac gcc gcg cac cag     144
Ser Ala Leu Arg Arg Thr Pro Gly Leu Asp Gly His Ala Ala His Gln
        35                  40                  45

tcg cag ctc gag atc gtg cag gag ctc ctc agc gac ccc acc gac gac     192
Ser Gln Leu Glu Ile Val Gln Glu Leu Leu Ser Asp Pro Thr Asp Asp
    50                  55                  60

gtc gtc gag ctc agc ggg tac agc ctc acc gtc cgt gac gtt gtc ggc     240
Val Val Glu Leu Ser Gly Tyr Ser Leu Thr Val Arg Asp Val Val Gly
65                  70                  75                  80

gcc gcc cgc aag ggg cgc agg gtc cgc gtc cag aac gac gac gag atc     288
Ala Ala Arg Lys Gly Arg Arg Val Arg Val Gln Asn Asp Asp Glu Ile
                85                  90                  95

cgc gca cgc gtc gac aag agc gtc gac ttc ctc aag gcc cag ctt cag     336
Arg Ala Arg Val Asp Lys Ser Val Asp Phe Leu Lys Ala Gln Leu Gln
            100                 105                 110

aac tcg gtc tac gga gtc acc acg g tgcgttccga gacgagaggc             381
Asn Ser Val Tyr Gly Val Thr Thr
        115                 120

ggaaatctcg ggatgccgca gcgctgaacg ctgacactcg cttggacggc tgccgcggtc  441

ttgcagg gt  ttc ggt ggc tcg gcc gac acg agg act gag gat gca gtc     489
        Gly Phe Gly Gly Ser Ala Asp Thr Arg Thr Glu Asp Ala Val
                    125                 130
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```
agc ctc cag aag gcg ctc atc gag cac cag ctc tgc ggc gtg acg ccg     537
Ser Leu Gln Lys Ala Leu Ile Glu His Gln Leu Cys Gly Val Thr Pro
135                 140                 145                 150

acg tcc gtc tcg tcc ttc agc gtc gga cgc ggc ctc gag aac acg ctt     585
Thr Ser Val Ser Ser Phe Ser Val Gly Arg Gly Leu Glu Asn Thr Leu
                155                 160                 165

ccg ctc gag gtc gtc cgc ggc gcc atg gtc atc cgc gtc aac tcg ctc     633
Pro Leu Glu Val Val Arg Gly Ala Met Val Ile Arg Val Asn Ser Leu
            170                 175                 180

acg cgt ggc cac tcg gcc gtc cgc ctc gtc gtc ctt gag gcg ctc acc     681
Thr Arg Gly His Ser Ala Val Arg Leu Val Val Leu Glu Ala Leu Thr
        185                 190                 195

aac ttc ttg aac cac cgc atc acg ccc atc gtc ccc ctc cgc ggc tcc     729
Asn Phe Leu Asn His Arg Ile Thr Pro Ile Val Pro Leu Arg Gly Ser
    200                 205                 210

atc tcg gcg tcg ggc gac ctc agc ccg ctc tcg tac atc gcc ggc gcc     777
Ile Ser Ala Ser Gly Asp Leu Ser Pro Leu Ser Tyr Ile Ala Gly Ala
215                 220                 225                 230

atc acc ggt cac ccc gac gtc aag gtt cac gtt ttg cac gag gga acc     825
Ile Thr Gly His Pro Asp Val Lys Val His Val Leu His Glu Gly Thr
                235                 240                 245

gag aag atc atg ttt gcg cgc gag gcc atc tcg ctc ttt ggt ctc gag     873
Glu Lys Ile Met Phe Ala Arg Glu Ala Ile Ser Leu Phe Gly Leu Glu
            250                 255                 260

gca gtc g gtacgtcgcg agtcctgact gcagtgagct gttcgagagt ctcccagttt    930
Ala Val

gctgactgcc ctttgttcat gcgattgcag tc  ctc ggc ccg aag gag ggt ctc    983
                                    Val Leu Gly Pro Lys Glu Gly Leu
                                                270
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ggt ctg gtc aac gga acg gcc gtc tcc gcc tcg atg gcg acc ctc agt   1031
Gly Leu Val Asn Gly Thr Ala Val Ser Ala Ser Met Ala Thr Leu Ser
        275                 280                 285

ctg cac gac tcg cac atg ctc tcg ctc ctc tcg cag gcc ttg acg gct   1079
Leu His Asp Ser His Met Leu Ser Leu Leu Ser Gln Ala Leu Thr Ala
    290                 295                 300

ctc acg gtg gag gcc atg gtc ggc cag cag ggc tcg ttc gcg ccg ttc   1127
Leu Thr Val Glu Ala Met Val Gly Gln Gln Gly Ser Phe Ala Pro Phe
305                 310                 315                 320

atc cac gac gtc tgc cgc ccg cac ccc ggc cag gtc gag gtc gcg cgc   1175
Ile His Asp Val Cys Arg Pro His Pro Gly Gln Val Glu Val Ala Arg
                325                 330                 335

aac atc cgc acg ctc ctt tcc ggc tcg tcg ttt gcc gtt gag cac gag   1223
Asn Ile Arg Thr Leu Leu Ser Gly Ser Ser Phe Ala Val Glu His Glu
            340                 345                 350

gag gag gtc aag gtc aag gac gac gag ggc att ctt cgc cag gac cgc   1271
Glu Glu Val Lys Val Lys Asp Asp Glu Gly Ile Leu Arg Gln Asp Arg
        355                 360                 365

tac ccg ctc cgc acg tcg cct cag gttcgtcccc tctctctccc cttccctccg  1325
Tyr Pro Leu Arg Thr Ser Pro Gln
    370                 375

tccgaccggc gcgtcgagac ttacgttttg cgtatccag ttc ctc ggc ccg ctc    1379
                                            Phe Leu Gly Pro Leu
                                                        380

gtg gag gac atg atg cac gcc tac tcg act ctc tcg ctc gag aac aac   1427
Val Glu Asp Met Met His Ala Tyr Ser Thr Leu Ser Leu Glu Asn Asn
            385                 390                 395

acg acg acc gac aac ccg ctc ctc gac gtc gag aac aag cag acc gcg   1475
Thr Thr Thr Asp Asn Pro Leu Leu Asp Val Glu Asn Lys Gln Thr Ala
        400                 405                 410
```

cac ggc ggc aac ttc cag gcg tcg gct gtc tcg att tcg atg gag aag 1523
His Gly Gly Asn Phe Gln Ala Ser Ala Val Ser Ile Ser Met Glu Lys
415 420 425

acc agg tgcgtctctc gctgccttcg tactccgatc ttgtgctgaa tgttcttctc 1579
Thr Arg
430

ctgcagg ctc gca ctc gcc ctc atc ggc aag ctc aac ttc acg cag tgc 1628
Leu Ala Leu Ala Leu Ile Gly Lys Leu Asn Phe Thr Gln Cys
435 440 445

acc gag ttg ctc aac gct gcc atg aac cgc ggc ctg cct tcg tgc ctc 1676
Thr Glu Leu Leu Asn Ala Ala Met Asn Arg Gly Leu Pro Ser Cys Leu
450 455 460

gct gcc gag gac ccg tcg ctc aac tat cac ggc aag ggc ttg gac att 1724
Ala Ala Glu Asp Pro Ser Leu Asn Tyr His Gly Lys Gly Leu Asp Ile
465 470 475

cac atc gct gct tac gct tcg gag gtgagccgtc gacgttctcc gccgtcgctc 1778
His Ile Ala Ala Tyr Ala Ser Glu
480 485

gtcccttca gcgcacccag gctgacttcc tttcctctg tag ctc ggc cac ctt 1833
Leu Gly His Leu

gcc aac ccg gtc act acc ttc gtc cag ccc gca gag atg ggc aac cag 1881
Ala Asn Pro Val Thr Thr Phe Val Gln Pro Ala Glu Met Gly Asn Gln
490 495 500 505

gcc gtc aac tcg ctc gct ctc atc tcc gcg cgc cgc act gcc gag gcc 1929
Ala Val Asn Ser Leu Ala Leu Ile Ser Ala Arg Arg Thr Ala Glu Ala
510 515 520

aac gac gtc ctt tct ctc gtgcgttcgt gtcgcaatga gtcccgacgc 1977
Asn Asp Val Leu Ser Leu
525

```
aatagcgact gactgcgcga tcctgagcag ctt ctc gcc tcg cac ctg tac tgc  2031
                                  Leu Leu Ala Ser His Leu Tyr Cys
                                  530                 535

acg ctc cag gcc gtc gac ctc cgc gcg atg gag ctc gac ttc aag aag  2079
Thr Leu Gln Ala Val Asp Leu Arg Ala Met Glu Leu Asp Phe Lys Lys
            540                 545                 550

cag ttc gac ccg ctt ctc ccg act ctc ctc cag cag cac ctc ggc act  2127
Gln Phe Asp Pro Leu Leu Pro Thr Leu Leu Gln Gln His Leu Gly Thr
        555                 560                 565

ggc ctc gac gtc aac gca ctt gcg ctc gag gtc aag aag gcg ctc aac  2175
Gly Leu Asp Val Asn Ala Leu Ala Leu Glu Val Lys Lys Ala Leu Asn
    570                 575                 580

aag cgt ctc gag cag acg acg acg tac gac ctc gag ccg cgc tgg cac  2223
Lys Arg Leu Glu Gln Thr Thr Thr Tyr Asp Leu Glu Pro Arg Trp His
585                 590                 595

gac gcc ttc tcg tac gcg acc ggc acc gtc gtc gag ctc ctc tcg tcc  2271
Asp Ala Phe Ser Tyr Ala Thr Gly Thr Val Val Glu Leu Leu Ser Ser
600                 605                 610                 615

tcg ccc tct gcc aac gtc acc ctt act gcc gtc aac gcg tgg aag gtt  2319
Ser Pro Ser Ala Asn Val Thr Leu Thr Ala Val Asn Ala Trp Lys Val
            620                 625                 630

gcc tcg gcc gag aag gcc atc tcg ctc acg cgc gag gtg cgc aac cgc  2367
Ala Ser Ala Glu Lys Ala Ile Ser Leu Thr Arg Glu Val Arg Asn Arg
        635                 640                 645

ttc tgg cag acg ccg tct tcg cag gcg ccg gcg cac gca tac ctc tcg  2415
Phe Trp Gln Thr Pro Ser Ser Gln Ala Pro Ala His Ala Tyr Leu Ser
    650                 655                 660

ccg cgc acg cgc gtc ctg tac tcg ttc gtg cgc gag gag ctc ggc gtg  2463
Pro Arg Thr Arg Val Leu Tyr Ser Phe Val Arg Glu Glu Leu Gly Val
665                 670                 675
```

cag gcg cgc cgc ggc gac gtg ttt gtc ggc gtg cag cag gag acg atc 2511
Gln Ala Arg Arg Gly Asp Val Phe Val Gly Val Gln Gln Glu Thr Ile
680 685 690 695

ggg agc aac gtc tcg cgc atc tac gag gcc atc aag gac ggc cgc atc 2559
Gly Ser Asn Val Ser Arg Ile Tyr Glu Ala Ile Lys Asp Gly Arg Ile
700 705 710

aac cac gtc ctc gtc aag atg ctc gcg taaggcccga gcaagcctcg 2606
Asn His Val Leu Val Lys Met Leu Ala
715 720

cctagacgcc cgcctcaccc caagaccagc ttttcgacgt cgtgtcgtgc caagaacgga 2666

ctttcctcca tacacatgtc gtcttactct ctcgccgtca tcacgtctct cagttctttc 2726

gtatcccgcg tctct 2741

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<211> 2163
<212> DNA
<213> Artificial Sequence

<220>
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theoretical sequence based in part on SEQ ID NO:20

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<221> CDS
<222> (1)..(2163)
<223>

<400> 29
atg gcc ccc tcc btc gac tcg atc gcg acc tcg btc gcc aac ggc btc 48
Met Ala Pro Ser Xaa Asp Ser Ile Ala Thr Ser Xaa Ala Asn Gly Xaa
1 5 10 15

dcv aac ggv thg cac gcc gct ccg hcc aag ycg scw acg ggc gcc acg 96
Xaa Asn Xaa Xaa His Ala Ala Pro Xaa Lys Xaa Xaa Thr Gly Ala Thr
20 25 30

tcc ach ctc mgm cgg ccg bcc dgg ctc gct cct ccc gcc acc cag vhg 144
Ser Xaa Leu Xaa Arg Pro Xaa Xaa Leu Ala Pro Pro Ala Thr Gln Xaa
35 40 45

```
acg cag ctc gac atc gtb gag vag atc ctc gcc gac ccc acc gac gac      192
Thr Gln Leu Asp Ile Xaa Glu Xaa Ile Leu Ala Asp Pro Thr Asp Asp
    50                  55                  60

gws vtc gaa ctc gac ggg tac acc ctc acc ctc ggh gac gtc gtc ggc      240
Xaa Xaa Glu Leu Asp Gly Tyr Thr Leu Thr Leu Xaa Asp Val Val Gly
65                  70                  75                  80

gcc gcb cgc aag ggc cgc hcb gtc cgc gtc cag aca gmc gac gag atc      288
Ala Ala Arg Lys Gly Arg Xaa Val Arg Val Gln Thr Xaa Asp Glu Ile
                85                  90                  95

cgc gca aag atc gac aav agb gtc gag ttc ctc cgb dcb cag ctc bac      336
Arg Ala Lys Ile Asp Xaa Xaa Val Glu Phe Leu Arg Xaa Gln Leu Xaa
            100                 105                 110

aac agb gtc tac ggh gtc acg act ggt ttc ggc ggc tcg gcc gac acc      384
Asn Xaa Val Tyr Xaa Val Thr Thr Gly Phe Gly Gly Ser Ala Asp Thr
        115                 120                 125

cgg act gag gat gcv atc tcg ctc cag aag gcb ctc ctc gag cac cag      432
Arg Thr Glu Asp Ala Ile Ser Leu Gln Lys Ala Leu Leu Glu His Gln
    130                 135                 140

ctc tgc ggt gtb ctc ccb acg tcg dtc gab tcc ttc vgc ctc ggh cgc      480
Leu Cys Gly Xaa Leu Xaa Thr Ser Xaa Xaa Ser Phe Xaa Leu Xaa Arg
145                 150                 155                 160

ggc ctc gag aac tcg ctt ccg ctc gag gtc gtc cgc ggc gcc atg acc      528
Gly Leu Glu Asn Ser Leu Pro Leu Glu Val Val Arg Gly Ala Met Thr
                165                 170                 175

atc cgc gtc aac tcg ctc acb cgc ggc cac tcg gcb gtc cgc ctc gtc      576
Ile Arg Val Asn Ser Leu Xaa Arg Gly His Ser Ala Val Arg Leu Val
            180                 185                 190

gtc ctc gag gcg ctc acc aac ttc ctc aac cac ggc atc acc ccc atc      624
Val Leu Glu Ala Leu Thr Asn Phe Leu Asn His Gly Ile Thr Pro Ile
        195                 200                 205

gtc ccc ctc cgc ggc acc atc tcg gcg tcg ggc gac ctc tcc ccb ctc      672
Val Pro Leu Arg Gly Thr Ile Ser Ala Ser Gly Asp Leu Ser Xaa Leu
    210                 215                 220

tcb tac atc gcc gcc gcc atc acc ggt cac ccg gac dbc aag gtb cac      720
Xaa Tyr Ile Ala Ala Ala Ile Thr Gly His Pro Asp Xaa Lys Xaa His
225                 230                 235                 240

gty kts cac gag ggc ams gag aag atc atg thc gcc cgc gag gcg atc      768
Xaa Xaa His Glu Gly Xaa Glu Lys Ile Met Xaa Ala Arg Glu Ala Ile
                245                 250                 255

gcg ctc ttb ggt ctc gag ccc gtc gtc ctc ggc ccg aag gag ggt ctc      816
Ala Leu Xaa Gly Leu Glu Pro Val Val Leu Gly Pro Lys Glu Gly Leu
            260                 265                 270

ggt ctc gtc aac ggc acg gcc gtc tcc gcc tcg atg gcg acc ctc gct      864
Gly Leu Val Asn Gly Thr Ala Val Ser Ala Ser Met Ala Thr Leu Ala
        275                 280                 285
```

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ctg cac gac gca cac atg ctc tcg ctc ctc tcg cag gcg ctc acg gct      912
Leu His Asp Ala His Met Leu Ser Leu Leu Ser Gln Ala Leu Thr Ala
    290                 295                 300

ctb acg gtc gag gcc atg gtc ggc cac gcc ggc tcg ttc cac ccv ttc      960
Xaa Thr Val Glu Ala Met Val Gly His Ala Gly Ser Phe His Xaa Phe
305                 310                 315                 320

ctc cac gac gtc acg cgc cct cac ccg acc cag atc gag gtc gcg cgc     1008
Leu His Asp Val Thr Arg Pro His Pro Thr Gln Ile Glu Val Ala Arg
                325                 330                 335

aac atc cgc acg ctc ctc gag ggc agc hvg ttt gcc gtc cac cac gag     1056
Asn Ile Arg Thr Leu Leu Glu Gly Ser Xaa Phe Ala Val His His Glu
            340                 345                 350

gag gag gtc aag gtc aag gac gac gag ggc att ctc cgc cag gac cgc     1104
Glu Glu Val Lys Val Lys Asp Asp Glu Gly Ile Leu Arg Gln Asp Arg
        355                 360                 365

tac ccg ctc cgc acg tcg cct cag tgg ctc ggc ccg ctc gtc agc gac     1152
Tyr Pro Leu Arg Thr Ser Pro Gln Trp Leu Gly Pro Leu Val Ser Asp
    370                 375                 380

atg att cac gcc cac gcb gtc ctc tcg ctc gag gcc gag tcg acg acc     1200
Met Ile His Ala His Ala Val Leu Ser Leu Glu Ala Glu Ser Thr Thr
385                 390                 395                 400

gac aac ccg ctc atc gac gtc gag aac aag ahg acc cac cac ggc ggc     1248
Asp Asn Pro Leu Ile Asp Val Glu Asn Lys Xaa Thr His His Gly Gly
                405                 410                 415

aac ttc cag gcg dcc gct gtc gcv aac acg atg gag aag act cgc ctc     1296
Asn Phe Gln Ala Xaa Ala Val Ala Asn Thr Met Glu Lys Thr Arg Leu
            420                 425                 430

gcv ctc gcc ctg atc ggc aag ctc aac ttc acg cag ctc acc gag atg     1344
Ala Leu Ala Leu Ile Gly Lys Leu Asn Phe Thr Gln Leu Thr Glu Met
        435                 440                 445

ctc aac gcc ggc atg aac cgc ggc ctb ccb tcc tgc ctc gct gcc gag     1392
Leu Asn Ala Gly Met Asn Arg Gly Xaa Xaa Ser Cys Leu Ala Ala Glu
    450                 455                 460

gac ccb tcg ctc tcc tat cac tgc aag ggc ctc gac att gcc gcb gcb     1440
Asp Xaa Ser Leu Ser Tyr His Cys Lys Gly Leu Asp Ile Ala Ala Ala
465                 470                 475                 480

gcb tac act tcg gag ctc ggh cac ctt gcc aac ccg gtb acg acc cac     1488
Ala Tyr Thr Ser Glu Leu Xaa His Leu Ala Asn Pro Xaa Thr Thr His
                485                 490                 495

gtc cag ccg gch gag atg ggc aac cag gcc gtc aac tcg ctc gcb ctc     1536
Val Gln Pro Arg Glu Met Gly Asn Gln Ala Val Asn Ser Leu Ala Leu
            500                 505                 510

atc tcg gcb cgc cgc acb gcc gag gcc aac gac gtc ctt tct ctc ctc     1584
Ile Ser Ala Arg Arg Xaa Ala Glu Ala Asn Asp Val Leu Ser Leu Leu
        515                 520                 525
```

```
ctc gcc acc cac ctc tac tgc gtb ctc cag gcc gtc gac ctc cgc gcg    1632
Leu Ala Thr His Leu Tyr Cys Xaa Leu Gln Ala Val Asp Leu Arg Ala
    530                 535                 540

atg gag ttc gag ttc aag aag cag ttc gac ccg vtb vtc vcb dcg ctc    1680
Met Glu Phe Glu Phe Lys Lys Gln Phe Asp Pro Xaa Xaa Xaa Xaa Leu
545                 550                 555                 560

htc vag cag cac ttt ggc dcy gcc ctc gac ggc wac gaa ctc ghg gac    1728
Xaa Xaa Gln His Phe Gly Xaa Ala Leu Asp Gly Xaa Glu Leu Xaa Asp
                565                 570                 575

aag gtc aac aag dcg ctc dac aag cgb ctc gag cag acc aac tcg tac    1776
Lys Val Asn Lys Xaa Leu Xaa Lys Arg Leu Glu Gln Thr Asn Ser Tyr
            580                 585                 590

gac ctc gag ccg cgc tgg cac gac gcc ttc tcg ttc gcg acc ggc acc    1824
Asp Leu Glu Pro Arg Trp His Asp Ala Phe Ser Phe Ala Thr Gly Thr
        595                 600                 605

gtc gtc gag ctc ctc tcg tcc tcg ccb yct gcc aag gtc tcg ctc gcb    1872
Val Val Glu Leu Leu Ser Ser Ser Xaa Xaa Ala Lys Val Ser Leu Ala
    610                 615                 620

gcc gtc aac gcc tgg aag gtc gcc tcc gcc gag aag gcc atc tcg ctc    1920
Ala Val Asn Ala Trp Lys Val Ala Ser Ala Glu Lys Ala Ile Ser Leu
625                 630                 635                 640

acg cgc bav gtc cgc gac hcc ttc tgg bcg gcb ccg tcg tcg tcg tcg    1968
Thr Arg Xaa Val Arg Asp Xaa Phe Trp Xaa Ala Pro Ser Ser Ser Ser
                645                 650                 655

ccc gcg ctc dcg tac ctc tcg ccg cgc acg cgc gtc ctg tac tcg ttc    2016
Pro Ala Leu Xaa Tyr Leu Ser Pro Arg Thr Arg Val Leu Tyr Ser Phe
            660                 665                 670

gtc cgc gag gag ctc ggc gtc aag gcc cgc cgc ggc gac gtc ttc ctc    2064
Val Arg Glu Glu Leu Gly Val Lys Ala Arg Arg Gly Asp Val Phe Leu
        675                 680                 685

ggc aag cag gag gtg acg atc ggc acc aac gtc tcc cgc atc tac gag    2112
Gly Lys Gln Glu Val Thr Ile Gly Thr Asn Val Ser Arg Ile Tyr Glu
    690                 695                 700

gcc atc aag dvc ggc hgc atc aac cac gtc ctc gtc aag atg ctc gcd    2160
Ala Ile Lys Xaa Gly Xaa Ile Asn His Val Leu Val Lys Met Leu Ala
705                 710                 715                 720

tag                                                                2163
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theoretical sequence based in part on SEQ ID NO:20

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<223> The 'Xaa' at location 12 stands for Val, Leu, or Phe.

<220>
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<222> (16)..(16)
<223> The 'Xaa' at location 16 stands for Val, Leu, or Phe.

<220>
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<223> The 'Xaa' at location 17 stands for Thr, Ala, or Ser.

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<223> The 'Xaa' at location 19 stands for Gly.

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<223> The 'Xaa' at location 20 stands for a stop codon, Ser, or Leu.

<220>
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<223> The 'Xaa' at location 25 stands for Thr, Pro, or Ser.

<220>
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<223> The 'Xaa' at location 27 stands for Pro, or Ser.

<220>
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<223> The 'Xaa' at location 28 stands for Ala, or Pro.

<220>
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<223> The 'Xaa' at location 34 stands for Thr.

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<223> The 'Xaa' at location 36 stands for Arg, or Ser.

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<223> The 'Xaa' at location 39 stands for Ala, Pro, or Ser.

<220>
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<223> The 'Xaa' at location 40 stands for Arg, Gly, or Trp.

<220>
<221> misc_feature
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<223> The 'Xaa' at location 48 stands for Lys, Thr, Met, Glu, Ala, Val, Gln, Pro, or Leu.

<220>
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<223> The 'Xaa' at location 54 stands for Val.

<220>
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<223> The 'Xaa' at location 56 stands for Lys, Glu, or Gln.

<220>
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<223> The 'Xaa' at location 65 stands for Glu, Asp, or Val.

<220>
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<223> The 'Xaa' at location 66 stands for Ile, Val, or Leu.

<220>
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<220>
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<223> The 'Xaa' at location 87 stands for Thr, Pro, or Ser.

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<223> The 'Xaa' at location 103 stands for Arg, or Ser.

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<223> The 'Xaa' at location 109 stands for Thr, Ala, or Ser.

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<223> The 'Xaa' at location 112 stands for Asp, His, or Tyr.

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<223> The 'Xaa' at location 114 stands for Arg, or Ser.

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<223> The 'Xaa' at location 154 stands for Glu, or Asp.

<220>
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<223> The 'Xaa' at location 157 stands for Ser, Gly, or Arg.

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<223> The 'Xaa' at location 159 stands for Gly.

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<223> The 'Xaa' at location 223 stands for Pro.

<220>
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<220>
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<223> The 'Xaa' at location 237 stands for Ser, Thr, Ile, Gly, Ala, Val,
Cys, or Phe.

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<223> The 'Xaa' at location 239 stands for Val.

<220>
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<223> The 'Xaa' at location 241 stands for Val.

<220>
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<223> The 'Xaa' at location 242 stands for Val, Leu, or Phe.

<220>
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<223> The 'Xaa' at location 246 stands for Lys, Asn, or Thr.

<220>
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<223> The 'Xaa' at location 251 stands for Tyr, Ser, or Phe.

<220>
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<223> The 'Xaa' at location 259 stands for Leu, or Phe.

<220>
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<223> The 'Xaa' at location 305 stands for Leu.

<220>
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<220>
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stop codon, Trp, or Ser.

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<220>
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<223> The 'Xaa' at location 421 stands for Thr, Ala, or Ser.

<220>
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<223> The 'Xaa' at location 457 stands for Leu.

<220>
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<223> The 'Xaa' at location 458 stands for Pro.

<220>
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<223> The 'Xaa' at location 466 stands for Pro.

<220>
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<223> The 'Xaa' at location 487 stands for Gly.

<220>
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<223> The 'Xaa' at location 493 stands for Val.

<220>
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<223> The 'Xaa' at location 518 stands for Thr.

<220>
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<223> The 'Xaa' at location 536 stands for Val.

<220>
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<223> The 'Xaa' at location 556 stands for Met, Ile, Val, or Leu.

<220>
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<222> (557)..(557)
<223> The 'Xaa' at location 557 stands for Ile, Val, or Leu.

<220>
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<223> The 'Xaa' at location 558 stands for Thr, Ala, or Pro.

<220>
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<220>
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<223> The 'Xaa' at location 561 stands for Ile, Leu, or Phe.

<220>
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<223> The 'Xaa' at location 562 stands for Lys, Glu, or Gln.

<220>
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<223> The 'Xaa' at location 567 stands for Thr, Ala, or Ser.

<220>
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<223> The 'Xaa' at location 572 stands for Asn, or Tyr.

<220>
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<223> The 'Xaa' at location 575 stands for Glu, Ala, or Val.

<220>
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<220>
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<220>
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<220>
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<220>
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<223> The 'Xaa' at location 643 stands for Glu, Asp, Gln, His, a stop codon, or Tyr.

<220>
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<223> The 'Xaa' at location 647 stands for Thr, Pro, or Ser.

<220>
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<223> The 'Xaa' at location 650 stands for Ala, Pro, or Ser.

<220>
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<222> (660)..(660)
<223> The 'Xaa' at location 660 stands for Thr, Ala, or Ser.

<220>
<221> misc_feature
<222> (708)..(708)
<223> The 'Xaa' at location 708 stands for Asn, Ser, Thr, Asp, Gly, Ala, Tyr, or Cys.

<220>
<221> misc_feature
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<223> The 'Xaa' at location 710 stands for Ser, Arg, or Cys.

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Met Ala Pro Ser Xaa Asp Ser Ile Ala Thr Ser Xaa Ala Asn Gly Xaa
1               5                  10                  15

Xaa Asn Xaa Xaa His Ala Ala Pro Xaa Lys Xaa Xaa Thr Gly Ala Thr
            20                  25                  30

Ser Xaa Leu Xaa Arg Pro Xaa Xaa Leu Ala Pro Pro Ala Thr Gln Xaa
        35                  40                  45

Thr Gln Leu Asp Ile Xaa Glu Xaa Ile Leu Ala Asp Pro Thr Asp Asp
    50                  55                  60

Xaa Xaa Glu Leu Asp Gly Tyr Thr Leu Thr Leu Xaa Asp Val Val Gly
65                  70                  75                  80

Ala Ala Arg Lys Gly Arg Xaa Val Arg Val Gln Thr Xaa Asp Glu Ile
                85                  90                  95

Arg Ala Lys Ile Asp Xaa Xaa Val Glu Phe Leu Arg Xaa Gln Leu Xaa
            100                 105                 110

Asn Xaa Val Tyr Xaa Val Thr Thr Gly Phe Gly Gly Ser Ala Asp Thr
        115                 120                 125
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Arg Thr Glu Asp Ala Ile Ser Leu Gln Lys Ala Leu Leu Glu His Gln
130 135 140

Leu Cys Gly Xaa Leu Xaa Thr Ser Xaa Xaa Ser Phe Xaa Leu Xaa Arg
145 150 155 160

Gly Leu Glu Asn Ser Leu Pro Leu Glu Val Val Arg Gly Ala Met Thr
165 170 175

Ile Arg Val Asn Ser Leu Xaa Arg Gly His Ser Ala Val Arg Leu Val
180 185 190

Val Leu Glu Ala Leu Thr Asn Phe Leu Asn His Gly Ile Thr Pro Ile
195 200 205

Val Pro Leu Arg Gly Thr Ile Ser Ala Ser Gly Asp Leu Ser Xaa Leu
210 215 220

Xaa Tyr Ile Ala Ala Ala Ile Thr Gly His Pro Asp Xaa Lys Xaa His
225 230 235 240

Xaa Xaa His Glu Gly Xaa Glu Lys Ile Met Xaa Ala Arg Glu Ala Ile
245 250 255

Ala Leu Xaa Gly Leu Glu Pro Val Val Leu Gly Pro Lys Glu Gly Leu
260 265 270

Gly Leu Val Asn Gly Thr Ala Val Ser Ala Ser Met Ala Thr Leu Ala
275 280 285

Leu His Asp Ala His Met Leu Ser Leu Leu Ser Gln Ala Leu Thr Ala
290 295 300

Xaa Thr Val Glu Ala Met Val Gly His Ala Gly Ser Phe His Xaa Phe
305 310 315 320

Leu His Asp Val Thr Arg Pro His Pro Thr Gln Ile Glu Val Ala Arg
325 330 335

Asn Ile Arg Thr Leu Leu Glu Gly Ser Xaa Phe Ala Val His His Glu
340 345 350

Glu Glu Val Lys Val Lys Asp Asp Glu Gly Ile Leu Arg Gln Asp Arg
355 360 365

Tyr Pro Leu Arg Thr Ser Pro Gln Trp Leu Gly Pro Leu Val Ser Asp
370 375 380

Met Ile His Ala His Ala Val Leu Ser Leu Glu Ala Glu Ser Thr Thr
385 390 395 400

Asp Asn Pro Leu Ile Asp Val Glu Asn Lys Xaa Thr His His Gly Gly
405 410 415

Asn Phe Gln Ala Xaa Ala Val Ala Asn Thr Met Glu Lys Thr Arg Leu
420 425 430

Ala Leu Ala Leu Ile Gly Lys Leu Asn Phe Thr Gln Leu Thr Glu Met
435 440 445

Leu Asn Ala Gly Met Asn Arg Gly Xaa Xaa Ser Cys Leu Ala Ala Glu
450 455 460

Asp Xaa Ser Leu Ser Tyr His Cys Lys Gly Leu Asp Ile Ala Ala Ala
465 470 475 480

Ala Tyr Thr Ser Glu Leu Xaa His Leu Ala Asn Pro Xaa Thr Thr His
485 490 495

Val Gln Pro Arg Glu Met Gly Asn Gln Ala Val Asn Ser Leu Ala Leu
500 505 510

Ile Ser Ala Arg Arg Xaa Ala Glu Ala Asn Asp Val Leu Ser Leu Leu
515 520 525

Leu Ala Thr His Leu Tyr Cys Xaa Leu Gln Ala Val Asp Leu Arg Ala
530 535 540

Met Glu Phe Glu Phe Lys Lys Gln Phe Asp Pro Xaa Xaa Xaa Xaa Leu
545 550 555 560

Xaa Xaa Gln His Phe Gly Xaa Ala Leu Asp Gly Xaa Glu Leu Xaa Asp
565 570 575

Lys Val Asn Lys Xaa Leu Xaa Lys Arg Leu Glu Gln Thr Asn Ser Tyr
580 585 590

Asp Leu Glu Pro Arg Trp His Asp Ala Phe Ser Phe Ala Thr Gly Thr
595 600 605

Val Val Glu Leu Leu Ser Ser Ser Xaa Xaa Ala Lys Val Ser Leu Ala
610 615 620

Ala Val Asn Ala Trp Lys Val Ala Ser Ala Glu Lys Ala Ile Ser Leu
625 630 635 640

Thr Arg Xaa Val Arg Asp Xaa Phe Trp Xaa Ala Pro Ser Ser Ser Ser
645 650 655

Pro Ala Leu Xaa Tyr Leu Ser Pro Arg Thr Arg Val Leu Tyr Ser Phe
660 665 670

Val Arg Glu Glu Leu Gly Val Lys Ala Arg Arg Gly Asp Val Phe Leu
675 680 685

Gly Lys Gln Glu Val Thr Ile Gly Thr Asn Val Ser Arg Ile Tyr Glu
690 695 700

Ala Ile Lys Xaa Gly Xaa Ile Asn His Val Leu Val Lys Met Leu Ala
705 710 715 720